GTIC-Biot ch/ChemLib

From: S nt: To:

Mertz, Prema Monday, July 15, 2002 9:08 AM STIC-Biotech/ChemLib

Subject:

09/521,195

Please search SEQ ID NO:2, 4 with DNA databases.

Please search SEQ ID NO:1, 3 with protein databases.

Thanks

Prema Mertz, Ph.D. Prema Mertz, Pri.D.
Primary Examiner
Art Unit 1646
Crystal Mall 1, Room 10E/01
United States Patent & Trademark Office
(703) 308-4229

CM7 Point of Contact.

CM7 Isoal Info Shears

Tel Specialist

Searcher:	
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TYPE OF SEARCH:								
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Mouse OCTN1 amino
A protein with cat
Human carnitine tr
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A protein with cat
Mouse OCTN2 amino
Mouse CTN3 protei
Drosophila melanog
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ALIGNMENTS

RESULT AAY01649 20-MAY-1998; 08-SEP-1997; Organic cation heart disease; A protein with cation transporting activity 23-JUN-1999 AAY01649; AAY01649 standard; Protein; 07-SEP-1998; W09913072-A1 Homo sapiens WPI; 1999-215062/18. N-PSDB; AAX26879. Nezu J, 18-MAR-1999 (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE Oku A; (first entry) transporter; OCT1; OCT2; drug development; fatty liver; cancer; anti-tumour drug; anticancer drug. 98JP-0156660. 97JP-0260972. 98WO-JP04009 551 AA

Genes homologous with organic cation transporters OCT1 and OCT2. useful in design of new drugs for treatment of diseases due to abnormality of the transporter functions

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RESULT
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       Organic cation
                      A protein with
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cancer;
       transporter; OCT1; OCT2; drug development; fatty liver;
                     cation transporting activity.
                                                                  Protein;
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anti-tumour drug;
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Pred. No. 3e-281
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08-SEP-1997;
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Pred. No. 5.4e-243;
99; Mismatches 44;
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Best Local Similarity
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541 dreespkvlitaf 553
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MRDYDEVIAFLGEWGPFQRLIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVPDAANLSS
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Pred. No. 5.4e-
99; Mismatches
                                                                                                                                                                                                                                                                  DB 21;
5.4e-243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1999
                                                                                              Genes homologous with organic cation transporters OCT1 and OCT2, useful in design of new drugs for treatment of diseases due to abnormality of the transporter functions {\bf r}
                                                                                                                                                                                   WPI; 1999-215062/18.
N-PSDB; AAX26880.
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08-SEP-1997;
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                                                            Claim 1; Page 51-55; 97pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transporter; cancer; anti-
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97JP-0260972
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The present sequence represents a protein with cation transporting activity. The genes are significantly homologous with organic cations are significantly considered by the cation of t

organic cation

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Best Local Similarity 75.9
Conservative
                                   Organic cation transportation; human; OCTN2; diagnosis; systemic carnitine of juvenile visceral steatosis.
                 Homo sapiens
                                                                       Human carnitine transporter
                                                                                            05-JUL-2000
                                                                                                                                  AAY83929
                                                                                                               AAY83929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transporters OCT1 and OCT2. The genes may used in drug development, particularly in the treatment of diseases due to abnormality of the organic cation transporter functions e.g. fatty liver, heart diseases and cancers, by controlling such as by inhibition or activation. Administration of anti-tumour and anticancer drugs in combination with a transporter protein inhibiting agent allows the agents to penetrate into the diseased cells to enhance the drug action.
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75.9%;
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                                                                       protein
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Pred. No. 2.8e
57; Mismatches
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l. No. 2.8e-217;
lismatches 71;
                                                                        OCTN2
                                         carnitine transporter protein; deficiency; mutation; gene ther
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                                          gene therapy;
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Best Local S
Matches 423
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                  481
                                                     421
                                                                                                                                                                                                                                                                                                                                                                                                         disease state.
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DSMETEENPKVL-ITAF
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423; Conserv
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                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                          57;
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2.8e-217;
nes 71;
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RESULT
ABG03029
                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CPR primers production of (II) and is sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II), (III) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful for treating CC diagning of sites expressing (II). (I) and (II) are useful for treating CC diagnostics, forensics, gene mapping, identification or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC amino acid sequences of the invention.

CC Note: The sequence data for this pattent did not appear in the printed CC at fip.wipo.int/pub/published_pct_sequences.
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                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                       Sequence
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DB; AAS67216.
 AWRNNSVPLRLRDGREVPHSCSRYRLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFS 120
                               mrdydevtaflgewgpfqrliffllsasiipngftglssvfliatpehrcrvpdaanlss 60
                                                   MRDYDEVIAFIGEWGPFQRLIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVPDAANLSS 60
                                                                                                       423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; SEQ ID No 33388; 103pp; English
                                                                                                      Conservative
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75.9%;
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Pred. No. 2.
                                                                                                      Mismatches
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2.8e-217;
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                                                                                                                                                                                                                                                                                                                                                                                 A protein with cation transporting activity.
                                    Genes homologous with organic cation transporters OCT1 auseful in design of new drugs for treatment of diseases abnormality of the transporter functions
                                                                                                                                                                                                                                                                                                                                        Organic cation heart disease;
                                                                                           WPI; 1999-215062/18
N-PSDB; AAX26902.
                                                                                                                                                                                       20-MAY-1998;
08-SEP-1997;
                                                                                                                                                                                                                                                                                      WO9913072-A1
                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY01652 standard; Protein; 557 AA.
             Claim 1; Page 75-79; 97pp; Japanese
                                                                                                                                                            (CHUG-) CHUGAI
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                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                       transporter; OCT1; OCT2; drug development; cancer; anti-tumour drug; anticancer drug.
                                                                                                                                                                                       98JP-0156660.
97JP-0260972.
                                                                                                                                                               RES INST MOLECULAR MEDICINE INC
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                                                    OCT1 and OCT2, seases due to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a protein with cation transporting activity. The genes are significantly homologous with organic cation transporters OCT1 and OCT2. The genes may used in drug development, particularly in the treatment of diseases due to abnormality of the organic cation transporter functions e.g. fatty liver, heart diseases and cancers, by controlling such as by inhibition or activation. Administration of anti-tumour and anticancer drugs in combination with a transporter protein inhibiting agent allows the agents to penetrate into the diseased cells to enhance the drug action.
                                            Mouse; transporter; OCTN1; identification; regulator;
                                                                                           Mouse OCTN2 amino acid sequence.
                                                                                                                          11-DEC-2000
                                                                                                                                                                                       AAB20580 standard; Protein; 557
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                                                                                                                                                                                                                                                                                                                      vylgaydrflpyilmgsltiltailtlffpesfgvplpdtidqmlrvkgikqwqiqsqtr
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                                                                                                                                                                                                                                                                                                                                                                                                                                              lsldtpnlhgdlyvncfilaavevpayvlawlllqylprrysisaalflggsvllfmqlv 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt kdvflstivtewdlvckddwkaplttslffvgvlmgsfisgqlsdrfgrknvlfltmgmq}
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                                                                                                                                                                                                                                                                                                                                                                                   pselfylstalvmvgkfgitsaysmvyvytaelyptvvrnmgvgvsstasrlgsilspyf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AWRNNSVPLRLRDGREVPHSCSRYRLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFS
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                                                                                                                         (first entry)
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72.9%;
                                               OCTN2; OCTN3; organic carnitine transport.
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Pred. No. 9.1e-212;
""smatches 75;
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The present invention describes a mouse organic cation transporter protein (CCTN3). Also described are: (1) a method for screening compounds for their ability to regulate the transport of an organic cation into the cell, by generating a cell expressing OCTN3 at the cell membrane, contacting with the compound and organic cation, and observing the degree of transport of the organic cation, and (2) a method for screening compounds for their ability to be transported into the cell by OCTN3, by generating a cell expressing OCTN3 at the cell membrane, contacting with the compound and observing the degree of transport of the compound. OCTN3 can be used for the identification of regulators of the transport of organic cations (especially carnitine) into cells by OCTN3, for use as drugs. The present sequence represents the mouse OCTN2 amino acid sequence, which is used in an example from
                                                                                                                                                                                                                                                                                                                                         Organic cation identification
Sequence
                                the present invention.
                                                                                                                                                                                                                                                                                                    Example 2; Fig 2; 58pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
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Matches Query Match Best Local Local Similarity 1 MRDYDEVIAFLGEWGPFQRLIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVPDAANLSS Conservative 76.1%; 72.9%; 70; Score 2164; DB 21; Pred. No. 9.1e-212; 70; Mismatches 75; Indels Length 6 Gaps 60

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В QΥ 뫄 20 밁 QΥ В Qy Вb QY В Q В QY DЬ 421 419 301 181 359 301 241 181 241 121 121 61 61 AKMNNTAVPAVIFD--SVEELNPLKQQKAFILDLFRTRNIAIMTIMSLILIMMLTSVGYFA lsldtpnlhgdiyvncfllaavevpayvlawlllqylprrysisaalflggsvllfmqlv VGYMLLPLFAYFIRDWRMLLLALTVPGVLCVPLWWFIPESPRWLISQRRFREAEDIIQKA TGFSFLQIFSISWEMETVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLGVCTFFA AWRNNSVPLRLRDGREVPHSCSRYRLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFS 120 LSLDAPNLHGDAYLNCFLSALIEIPAYITAWLLLRTLPRRYIIAAVLFWGGGVLLFIQLV fgfmvlplfayfirdwrmlllaltvpgvlcgalwwfipesprwlisggrikeaeviirka tgfsflqvfsvnfemftvlfvlvgmgqisnyvaafvlgteilsksiri|ifatlgvcifya awrnhsipletkdgrqvpqkcrryrlatianfselglepgrdvdleglegescldgweyd 120 420 418 300 240 300 240

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCTN2; diagnosis; systemic c
juvenile visceral steatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse carnitine transporter
                                                                                                                                                                                                                                 This sequence represents the mouse carnitine transporter protein OC The coding sequence of the corresponding human protein can be used target for diagnosis of systemic carnitine deficiency by detecting presence of mutations in the sequence, especially seen in the diseafuvenile wisceral steatosis (jvs). The wild type OCTN2 gene can be
                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                       MRDYDEVIAFLGEWGPFQRLIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVPDAANLSS
                                                                               AWRNINSVPLRLRDGREVPHSCSRYRLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFS
                                                                                                          TGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLGVCTFFA
                               QDVYLSTVVTEWNLVCEDNWKVPLTTSLFFVGYLLGSFVSGQLSDRFGRKNVLFATMAVQ
                                                                     {\tt awrnhsipletkdgrqvpqkcrryrlatianfselglepgrdvdleqleqescldgweyd}
                                                                                                                                                                                                                                                                                                                 transporter,
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                                                                                                                                                    Conservative
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72.9%;
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Pred. No. 9.1e-212;
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diagnostic
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      The present invention describes a mouse organic cation transporter protein (OCTN3). Also described are: (1) a method for screening compounds for their ability to regulate the transport of an organic cation into the cell, by generating a cell expressing OCTN3 at the cell membrane, contacting with the compound and organic cation, and observing the degree of transport of the organic cation; and (2) a method for screening compounds for their ability to be transported into the cell by OCTN3, by generating a cell expressing OCTN3 at the cell membrane, contacting with the compound and observing the degree of transport of the compound. OCTN3 can be used for the identification of
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                                                                                                                                                         Organic cation identification
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                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                         23-MAR-2001; 2001WO-US09231
                                                                                                                     WO200171042-A2
                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                       pharmaceutical.
                                                                                                                                                                                                                         Drosophila; developmental
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Pred. No. 1.5e-198;
5; Mismatches 85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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genes from Drosophila and
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                      glgassmvarvggilapylkllgeiwrplpliicgalsltagllslllpetinkpmpeti
                                         ilcgtmmvagisllatifvpsdmnwlivacamigklaitssygtiyifsaeqfptvvrnv
                                                                                                                                                                                                                                                                                                               rkptffaslv1q11fgvlaavapeyfsytisrmivgattsgvf1vayvlalemvgssyr-
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DB; ABL06382.
EQMQKVKWFRSGKKTRDSMETEE 542
                                                                                                              IIAAVLFWGGGVLLFIQLVPVDYYFLSIGLVMLGKFGITSAFSMLYVFTABLYPTLVRNM
                                                                                                                                        rktlliffdwfvnsgvyyglswntnnlggnqlvnfmisgaveipgytl|llftlnrwgrrs
                                                                                                                                                                   IMTIMSLLLWMLTSVGYFALSLDAPNLHGDAYLNCFLSALIEIPAYITAWLLLRTLPRRY
                                                                                                                                                                                                  rkdeafviiekaakenkvevpneiyeglvdevaekkkqdemaasqpaatvfdllrypnlr
                                                                                                                                                                                                                          RFREAEDIIQKAAKMNNTAVPAVIFDS-VEELNPLKQQ------KAFILDLFRTRNIA
                                                                                                                                                                                                                                                         lfagvamgmffsvgfmltagfayfihdwrwlgiaitlpgllflcyywilpesarwllmkg
                                                                                                                                                                                                                                                                                     IFSTLGVCTFFAVGYMLLPLFAYFIRDWRMLLLALTVPGVLCVPLWWFIPESPRWLISQR 288
                                                                                                                                                                                                                                                                                                                                            RKNVLFATMAVQTGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAWRNNSVPLRLRDGREVPHSCSRYRLATIANFSALGLEPGRDVDL- ----GQL-----
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001
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                                                                                                                                                                                                                                                                                                                    (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 31854; 21pp + Sequence Listing; English
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                                                                                                                                             EQESCLDGWEESQDVYLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQLSDRFG
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rkpilfaslviqvlfgvla--gvapeyftytfarlmvgattsgvflvayvvamemvgpdk
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PE
                       RKNVLFATMAVQTGFSFLQIFSISWEMFTVLF--VIVGMGQISNYVVAFILGTEILGKSV
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Pred. No. 1.5e
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15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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DB; AAK51500.
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Wang D,
Yang Y,
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Wejhrman T, Goodrich R;
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The invention relates to polynucleotides (AAK51456-AAK53435) and

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Human;
                                                                                                                                Human ORFX ORF2802 polypeptide sequence SEQ ID NO:5604.
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Pred. No. 2.4e-72;
18; Mismatches 221;
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Similarity 32.9 84; Conservative

27.48; 113;

Score 779.5; DB 1 Pred. No. 1.6e-70; 13; Mismatches 214

214; 21;

Indels Length

Gaps

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DAANLS 49;

FQRLIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVP-----

fqrvlyficafqniscgihylasvfmgvtphhvcrppgnvsqvvfhnhsnwsledtgall 61

Sequence

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cc which represent the human ORFX open reading frames I to 3161. The ORFX CS sequences have activities such as: cytostatic; hepatotropic; vulnerary: cc antipsoriatic; anticarvitatics antiarthritic; hepatotropic; vulnerary: cc antipsoriatic; anticarvitatic; antiarthritic; meuroprotective; costeopathic; anticarvitatic; antiarthritic; coagulant; vasotropic; cc antidiabetic; hypotensive; dermatological; immunosuppressant; cc antihiflammatory; antibacterial; antiviral; antifungal; antirheumatic; cc antihiflammatory; antibacterial; antiviral; antifungal; antirheumatic; cc antihipsorid; and antianaemic. The sequences can be used for determining cc the presence of or predisposition to, or preventing or treating cc pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy certors. The proteins and nucleic acids may be used to treat cancers, cc proliferative disorders, neurodegenerative disorders, osteoarthritis, cc proteins on hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, cc allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, cc coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotec anticonvulsant; osteopathic; antiarthritic; immunosuppressant; car immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antifheumatic; antithyroid; antiviral; antibacterial; antifungal; antifierative disorder; hypothec neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; A cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 4791-4792; 5507pp; English.
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25-APR-2000;
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of 251 novel human polypeptides encoded by a bone marrow-expressed polynucleotide. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2hao
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/AB_COMB.pep:*
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APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
TITLE OF INVENTION: Transport protein Which Effects The
TITLE OF INVENTION: Transport Of Cationic Xenoblotics and or Pharmaceuticals,
TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
              ATTORNEY/AGENT INFORMATION:
NAME: O'CONDOI, Steven p
REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 240
     TELECOMMUNICATION
                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                         CLASSIFICATION:
                                                                                                                                                                                                                  COUNTRY:
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                                                                                     March 18,
     INFORMATION:
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Patent No. 60636;
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; MOLECULE TYPE: peptide US-09-040-444-3
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APPLICANT: Koepsell, Hermann

APPLICANT: Grundeman, Dirk

APPLIC
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TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 555 amino acids
                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFWGGGVLLFIQLVPVDYYFLSIGLVMLGKFGITSAFSMLYVFTAELYPTLVRNMAVGVT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYNWFTSSVLYQGLIMHM-GLAGDNIYLDFFYSALVEFPAAFMIILIIDRIGRRYPWAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAEDIIQKAAKMNNTAVPAVI-----FDSVEELNPLKQQKAFILDLFRTRNIAIMTIMS 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIFYQVAYTVGLLVLAGVAYALPHWRWLQFTVALPNFFFLLYYWCIPESPRWLISQNKNA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDGWEFSQDVYLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQLSDRFGRKNVL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGWSPAEELNYTVPGPGPAGEASPROCRRYEVDWNOSTFDCVDPLASIDTNRSRLPLGPC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDVLEHGGEFHFFQKQMFFLLALLSATFAP---IYVGIVFLGFTPDHRCRSPGVAELSLR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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1300 I Street,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 702; DB 3;
Pred. No. 5.6e-65;
     Suite
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-501-572-1
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REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02481.1453-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4400
TELEPAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
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Best Local Similarity
Matches 184; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                            163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
                                                                                                                                                                392 LRTLPRRYIIAAVLFWGGGVLLEIQLVPVDYYFLSIGLVMLGKFGITSAFSMLYVFTAEL 451
                                                                                                                                                                                                                                                        332 LFRTRNIAIMTIMSLLLWMLTSVGYFALSLDAPNLHGDAYLNCFLSALIEIPAYITAWLL 391
                                                                                                                                                                                                                                                                                            278 LYYWFVPESPRWLLSQKRTTRAVRIMEQIAQKNGKVPPADLKMLCLEEDASEKRSPSFAD
                                                                                                                                                                                                                                                                                                                                                                    223 TLITEFVGSGYRRTTAILYQMA-----FTVGLVGLAGVAYAIPDWRWLQLAVSLPTFLFL
                                                                                                                                                                                                                                                                                                                                                                                                   216 ILGTEILGKSVR----IIFSTLGVCTFFAVGYMLLPLFAYFIRDWRMLLLALTVPGVLCV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 GLEPGRDVDLGQLEQESCLDGWEFSQDVYLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLGP------CEHGWVY--DTPGSSIVTEFNLVCGDAWKVDLFQSCVNLGFFL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRDYDEVIAFIGEWGPFQRLIFFLL---SASIIPNGFNGMSVVFLAGTPEHRCRVPDAAN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                          GSLVVGYIADRFGRKLCLLVTTLVTSVSGVLTAVAPDYTSMLLFRLLQGMVSKGSWVSGY 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSS--AWR-----ATIANFSAL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPTVDDVLEQVGEFGWFQKQAFLLLCLISASLAP - - - IYVGIVFLGFTPGHYCQNPGVAE
                                                                                                                                                                                                                                                                                                                               PLWWFIPESPRWLISQRRFREAEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQQKAFILD 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSFVSGQLSDRFGRKNVLFATMAVQTGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSQRCGWSQAEELNYTVPGLGPSDEASFLSQCMRYEVDWNQSTLDCVDPLSSLVANRSQL 117
                                                                                              YPTLVRNMAVGVTSTASRVGSIIAPYFVY-LGAYNRMLPYIVMGSLTVLIGIFTLFFPES
                                                                                                                                               IDRIGRIYPIAASNLYTGAACLLMIFIPHELHWLNYTLACLGRMGATIYLEMVCLYNAEL
                                                                                                                                                                                                                     LFRTPNLRKHTVILMYLWFSCAVLYQGLIMHVGATGANLYLDFFYSSLVEFPAAFIILVT
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 KGVALPETIEEAENL 532
                                  LGMTLPETLEQMQKV 525
                                                                     YPTFIRNLGMMVCSALCDLGGIFTPFMVFRLMEVWQALPLILFGVLGLTAGAMTLLLPET
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.2%; Score 687.5; DB 3; 33.2%; Pred. No. 1.9e-63; tive 88; Mismatches 230;
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US-09-040-444-1
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.2%;
Best Local Similarity 33.2%;
Matches 184; Conservative 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202)408-440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Grundeman, Dirk
APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport t
TITLE OF INVENTION: DNA Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: O'CONNOY, Steven P
REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 246
TELECOMMUNICATION INFORMATION:
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LENGTH: 556 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
 278
                                                                      223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                           96 GLEPGRDVDLGQLEQESCLDGWEFSQDVYLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLL 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                   1 MPTVDDVLEQVGEFGWFQKQAFLLLCLISASLAP---IYVGIVFLGFTPGHYCQNPGVAE
                                                                                                                                                                                                                                                                                                                                                                                    1 MRDYDEVIAFLGEWGPFQRLIFFLL---SASIIPNGFNGMSVVFLAGTPEHRCRVPDAAN
LYYWFVPESPRWLLSQKRTTRAVRIMEQIAQKNGKVPPADLKMLCLEEDASEKRSPSFAD
                               PLWWFIPESPRWLISQRRFREAEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQQKAFILD 331
                                                                ILGTEILGKSVR----IIFSTLGVCTFFAVGYMLLPLFAYFIRDWRMLLLALTVPGVLCV
                                                                                                                                                                        GSFVSGQLSDRFGRKNVLFATMAVQTGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAF 215
                                                                                                                                                                                                                                                                                {\tt LSQRCGWSQAEELNYTVPGLGPSDEASFLSQCMRYEVDWNQSTLDCVDPLSSLVANRSQL}
                                                                                                                                                                                                                                                                                                   LSS--AWR-----ATIANFSAL
                                                                                                                                         GSLVVGYTADRFGRKLCLLVTTLVTSVSGVLTAVAPDYTSMLLFRLLQGMVSKGSWVSGY
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(202)408-4400
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Pred. No. 1.9e-63;
8; Mismatches 230;
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US-08-501-572-2
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                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2,
                                                                                                           Matches 192;
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APPLICANT: Koepse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Transport protein Which Effects The TITLE OF INVENTION: Transport Of Cationic Xenobiotics and or Pharmaceuticals, INTITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
                                                                                                                                                                                                                                                                                                                                                                   NAME: Toohey, Kimberlin M
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02481.1453-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
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58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                LENGTH: 553 amino acids
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                                                                      MRDYDEVIAFLGEWGPFQR---LIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVPDAAN 57
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LSS--AWR-----NNSVPLRLRDGREVPHSCSRYR------
                                     MPTVDDILEQVGESGWFQKQAFLILCLLSAAFAP---ICVGIVFLGFTPDHHCQSPGVAE
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Gorboulev, Valentin
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linear
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                                                                                                         23.9%; Score 680; DB 3; 33.4%; Pred. No. 1.1e-62; tive 85; Mismatches 228
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                                                                                                             228;
                                                                                                                                             Length 553
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                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,444
FILING DATE: MATCh 18, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: O'CONNOY, Steven P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                       TELEFAX: (202)408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                     ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                           REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
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                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                             CITY: Wa
STATE: I
COUNTRY:
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                                                                                                                           NAME: O'Connor, Steven P
REGISTRATION NUMBER: 41,225
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                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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553 amino acids
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Gorboulev, Valentin
                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                           (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport protein Which Effects The Transport Of Cationic Xenobiotics ar DNA Sequences Encoding It And Their
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18, 1998
                                                                                                                 2481.1453-01
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single

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; TYPE: amino acid
; STRANDENNESS: sinc
; TOPOLOGY: linear
; MOLECULE TYPE: pept:
US-09-040-444-2
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Best Local Similarity
                                                                                                                                                                                                                                                                      Sequence 2, Applicati Patent No. 5972702 GENERAL INFORMATION:
                                                                                                                                                                                                     APPLICANT: Beier, David R.
APPLICANT: Brady, Kevin P.
TITLE OF INVENTION: OSTEOCLAST TRANSPORTER
NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273
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                                                                                                                                                                                                                                                                                                                                                                                           511 LLPETKGDALPETMKDAENL----GRKAKPKENT 540
                                                                                   CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPTVDDILEQVGESGWFQKQAFLILCLLSAAFAP---ICVGIVFLGFTPDHHCQSPGVAE
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                                                                                                                                                                                                                                                                                                                                                                                                                          FFPESLGMTLPETLEQMQKVKWFRSGKKTRDSMET 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAWLLLRTLPRRYIIAAVLFWGGGVLLFIQLVPVDYYFLSIGLVMLGKFGITSAFSMLYV 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFILDLFRTRNIAIMTIMSLLLWMLTSVGYFALSLDAPNLHGDAYLNCFLSALIEIPAYI 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LWWFIPESPRWLISQRRFREAEDIIQKAAKMNNTAVPAVI-----FDSVEELNPLKQQK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGTEIIG----KSVRIIFSTLGVCTEFAVGYMLLPLFAYFIRDWRMLLLALTVPGVLCVP 272
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; Pred. No. 1.1e-62;
85; Mismatches 228
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US-08-964-127-2
Sequence 2, Application
Patent No. 6277565
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Best Local Similarity
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LENGTH: 537 amino acids
TYPE: amino acid
TOPOLOGY: linear
GENERAL INFORMATION:
APPLICANT: Grandearl, Andrew David John
TITLE OF INVENTION: NOVEL GENES ENCODIN
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION UNMBER: 31,616
REFERENCE/DOCKET NUMBER: B00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 NNSVPLRLRDGREVPHSCSRY---RLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AASGSSAAFSPSLTVYMIFRFLCGCSISGISLSTIILNVEWVPTSTRAISSTTIGYC--Y
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                                                                                                                                                                                                                                                                                                                   LFIQLVPVDYYFLSIGLVMLGKFGITSAFSMLYVFTAELYPTLVRNMAVGVTSTASRVGS
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                                                                                                                                                                                                                               MIAPLVKITGELQPFIPNVIFWTMTLLGGSAAFFLLETLNRPLPETIEDIQ--DWYQQTK
                                                                                                                                                                                                                                               IIAPYFVYLGAYNRMLPYIVMGSLTVLIGIFTLFFPESLGMTLPETLEQMQKVKWFRSGK
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617-720-2441
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ilarity 30.0%; pred. No. 1.9e-57;
Conservative 102; Mismatches 245;
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                                                                                US/08964127
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                    ENCODING TRANSPORTER-LIKE
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12;

COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

OPERATING SYSTEM: SOFTWARE: FastSEC COMPUTER:

IBM Compatible SYSTEM: Windows 95

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: Fish & Richardson
STREET: 225 Franklin Street

STREET: 225 | CITY: Boston

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Query Match 9.4%; Score 267; DB 4; Best Local Similarity 23.4%; Pred. No. 2.1e-19; Matches 117; Conservative 88; Mismatches 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
                                                                                                                                                        400 IIAAVLFWGGGVLLFIQLVPVDYYFLSIGLVMLGKFGITSAFSMLYVFTAELYPTLVRNM 459
                                                                                                                                                                                                      322 RHCYQPVGGGGSPSDFYLCSLLA---SGTAALACVFLG--VTVDRFGRRGILLLSMTLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 ISWEMETVLEVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLGVCTFFAVGYMLLPLFA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 RLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFSQDVYLST-VVTEWNLVCEDNWKVP 143
                                                                     AVGVTSTASRVGSIIAP-YFVYLGAYNRMLPYIVMGSLTVLIGIFTLFFPESLGMTLPET
                           GLGLIMALGALGGLSGPAQRLHMG-HGAFLQHVVLAACALLCILSIMLLPETKRKLLPEV 486
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                                                                                                                                                                                                                                                                                              QMLGEEAQEAL -- QDLENTCPLPATSSFSFASLLNYRNI ----WKNLLILGFTNFIAHAI
                                                                                                                                                                                                                                                                                                                                   ---- NTAVPAVIFDSVEELNPLKQQKAF-ILDLFRTRNIAIMTIMSLLLWMLTS-----
                                                                                                                                                                                                                                                                                                                                                                                   LVSKDWRFLQRMITAPCILFLFYGWPGLFLESARWLIVKRQIEEAQSVLRILAERNRPHG
                                                                                                                 IASLVLL---GLWDYLNEAAITTF-----SVLGLFSSQAAAILSTLLAAEVIPTTVRGR 427
                                                                                                                                                                                                                                                -----VG-----YFALSLDAPNLHGDAYLNC-FLSALIEIPAYITAWLLLRTLPRRY 399
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-09-496-692-2
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US-09-496-692-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 9.4%; Score 267; DB 4; IBest Local Similarity 23.4%; Pred. No. 2.1e-19; Matches 117; Conservative 88; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09496692 Patent No. 6313271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Crews, Ph.D., L. Lee REGISTRATION NUMBER: P-43,5
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastsEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 520 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE TITLE OF INVENTION: MOLECULES
268 QMLGEEAQEAL--QDLENTCPLPATSSFSFASLLNYRNI----WKNLLTLGFTNFIAHAI
                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                       144 LTTSLFFVGVLLGSFVSGQLSDRFGRKNVLFATMAV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 000154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 LRDGELCRRPSLLRQPPPTR 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519
                                                                                                                                                                                                                                                                                                                                                   50 RVATSTDPSCSGFAPP-----DFNHCLKDWDYNGLPVLTTNAIGGWDLVCDLGWQVI 101
                                                                                                                                                                                                                                                                                                                                                                                          85 RLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFSQDVYLST-VVTEWNLVCEDNWKVP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 61//542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                LVSKDWRFLQRMITAPCILFLFYGWPGLFLESARWLIVKRQIEEAQSVLRILAERNRPHG 267
                                                                                                                                                                                                             ISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLGVCTFFAVGYMLLPLFA 250
                                                                                                                                                                                                                                                             LEQILFILGFASGYLFLGYPADRFGRRGIVLLTLGLVGPCGVGGAAAGSSTGVMALR--- 158
                                                                                                                              YFIRDWRMLLLALTVPGVLCVPLWW--FIPESPRWLISQRRFREAEDIIQKAAKMN----
                                                                                                                                                                      -----FLLGFLLAGVD-----LGVYLMRLELCDPTQRLRVALAGELVGVGGHFLFLGL-A 207
                                         ----NTAVPAVIFDSVEELNPLKQQKAF-ILDLFRTRNIAIMTIMSLLLWMLTS-----
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 520 amino acids TYPE: amino acids
TOPOLOGY: linn-

REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEPHONE: 61//542-8906

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567

APPLICATION NUMBER: US/0 FILING DATE: 06-NOV-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER:

MOLECULE TYPE: FRAGMENT TYPE:

protein internal

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US-09-031-392-5
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 115; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & Richardson P.C.
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TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tarta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 AVGVTSTASRVGSIIAP-YFVYLGAYNRMLPYIVMGSLTVLIGIFTLFFPESLGMTLPET
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                                                                   103
                                                                                                                                                                                                                                133 NLVCEDNWKVP------LTTSLFFVGVLLGSFVSGQLSDREGRKN--VLFATMAV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 RHCYQPVGGGSPSDFYLCSLLA---SGTAALACVFLG--VTVDRFGRRGILLLSMTLTG
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233
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ZIP: 02110-2804
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LGVCTFFAVGYMLLPLFAYFI----RDWRMLLLALTV-PGVLCVPLWWFIPESPRWLISQ 287
                                                            AGGCLMGFCKI-AESVEMLILGRLIIGLFCGLCTGFVPMYI--GEISPTALRGAFGTLNQ 159
                                                                                                                            QTG--FSFLQIFSISWEMFTVLFVIVGM--GQISNYVVAFILGTEILGKSVRIIFST--- 232
                                                                                                                                                                                            NYTLEERSETPPSSVLLTSLWSLSVAIFSVGGMIGSFSVGLFVNRFGRRNSMLIVNLLAI 102
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                                                                                                                                                                                                                                                                                                                                Conservative
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26-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                         8.2%;
                                                                                                                                                                                                                                                                                                                         ; Score 234.5; DB 2;
; Pred. No. 5.1e-16;
76; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                         Length 494;
                                                                                                                                                                                                                                                                                                                             Indels 109;
                                                                                                                                                                                                                                                                                                                         Gaps
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US~09-299-549-5
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; MOLECULE TYPE: US-09-299-549-5
                                                                                                                            PRIOR DATE: 26-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
FILING DATE: 26-FEB-1998
ATTORREY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/0720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09299549 Patent No. 6136547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tartag
APPLICANT: Weng,
                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
                                                                                                                                                                                                                                                                                                                                     SUFTWARE: PASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/299,549 FILTING NOWNER: US/09/299,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 -LVMLGKFGITSAFSMLYVFTAELYPTLVRNMAVGVTSTAS-----RVGSIIAPYFVYLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 ILVFVAFFEIGPG-PIPWFIVAELFGQGPRPAAMAVAGCSNWTSNFLVGLLFPSATFYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 GVVNTIFTVVSVFLVERAGRRTL--HLIGLGGMAFCSILMTISLLLKDNYSWMSFICIGA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 NYRQPIIISIMLQLSQQLSGINAVFYYSTGI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 RRFRE-----AEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQQKAFILDLFRTR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: M
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CO.
OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & ....
evrREET: 225 Franklin Street
                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------AWLILRTLPRRYIIAAVLFWGG----GVLLFIQLVPVDYY----FLSIG-
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                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tartaglia, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fish & Richardson P.C.
                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nux
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                                                                                                                                                                                                                                                                                                                                                                                                    Windows95
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                                                                                                                                                                                                   07334/072002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428
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Query Match 8.2 Best Local Similarity 25.2 Matches 115; Conservative

8.2%; Score 234.5; DB 4 25.2%; Pred. No. 5.1e-16; tive 76; Mismatches 156

DB 4; 156;

Length 494; Indels 109;

Gaps

23;

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133 43

23;

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Sequence 5, Application US/09610417 Patent No. 6346374 GENERAL INFORMATION:
                                                                                             INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION UMBER: US/09/610,417

FILING DATE: 05-Jul-2000

PRIOR APPLICATION NUMBER: 09/299,549

FILING DATE: <Unknown>
APPLICATION NUMBER: 09/299,549

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

THEORY OF THE PROPERTY OF THE PROPE
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 07334/072002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                           SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tartaglia, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRFRE-----AEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQQKAFILDLFRTR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCLMGFCKI-AESVEMLILGRLIIGLFCGLCTGFVPMYI--GEISPTALRGAFGTLNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYTLEERSETPPSSVLLTSLWSLSVAIFSVGGMIGSFSVGLFVNRFGRRNSMLIVNLLAI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLVCEDNWKVP------LTTSLFFVGVLLGSFVSGQLSDRFGRKN--VLFATMAV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYNRMLPYIVMGSLTVLIGIFTLF-FPESLGMTLPE 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY----VFIVFTVFLVIFWVFTFFKVPETRGRTFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILVEVAFFEIGPG-PIPWFIVAELFGQGPRPAAMAVAGCSNWTSNFLVGLLFPSATFYLG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVVNTJFTVVSVFLVERAGRRTL--HLIGLGGMAFCSILMTISLLLKDNYSWMSFICIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NYROPIIISIMLOLSQOLSGINAVFYYSTGI-----FKDAGVQEPVYATIGA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-----TAIMTIMSLLLWMLTSVGYFALSLDAPNLHGDAYLNCFLSALIEIPAYIT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGVCTFFAVGYMLLPLFAYFI----RDWRMLLLALTV-PGVLCVPLWWFIPESPRWLISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LVMLGKFGITSAFSMLYVFTAELYPTLVRNMAVGVTSTAS-----RVGSIIAPYFVYLG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AWLLIRTLPRRYIIAAVLFWGG----GVILFIQLVPVDYY----FLSIG- 428
TYPE: amino acid
                                                                                                                                                        TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEIC ACID MOLECULES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID
US-09-610-417-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-355-844-3; Sequence 3, A
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Matches 115; Conser
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pischbarg, Jo
APPLICANT: Czegledy, Fer
APPLICANT: Iserovich, Pa
APPLICANT: Li, Jun
APPLICANT: Li, Jun
APPLICANT: Cheung, Min
TITLE OF INVENTION: A ME
TITLE OF INVENTION: STRU
                    SOFTWARE: Patentin Release #1.0, CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,844
FILING DATE: 14-DEC-1994
CLASSIFICATION: 436
CLASSIFICATION: 436
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429
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                                                                                                                                                                                                                                                                                                                                                                                 STREET: 30 ROC
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKEEEKAKEILQRLWGTEDVAQDIQEMKD------ESMRMSQEKQVTVLELFRAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYNRMLPYIVMGSLTVLIGIFTLF-FPESLGMTLPE 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LVMLGKFGITSAFSMLYVFTAELYPTLVRNMAVGVTSTAS-----RVGSIIAPYFVYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVVNTIFTVVSVFLVERAGRRTL--HLIGLGGMAFCSILMTISLLLKDNYSWMSFICIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-----IAIMTIMSLLLWMLTSVGYFALSLDAPNLHGDAYLNCFLSALIEIPAYIT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRFRE-----AEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQQKAFILDLFRTR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGI----VIGILVAQIFGLKVILGTEDLWPLLLGFTILPAIIQCAALPFCPESPRELLIN 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGVCTFFAVGYMLLPLFAYFI----RDWRMLLLALTV-PGVLCVPLWWFIPESPRWLISQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGCLMGFCKI-AESVEMLILGRLIIGLFCGLCTGFVPMYI--GEISPTALRGAFGTLNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTG--FSFLQIFSISWEMFTVLFVIVGM--GQISNYVVAFILGTEILGKSVRIIFST---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYTLEERSETPPSSVLLTSLWSLSVAIFSVGGMIGSFSVGLFVNRFGRRNSMLIVNLLAI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYROPIIISIMLOLSOOLSGINAVFYYSTGI-----FKDAGVQEPVYATIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Application US/08355844 5940307
                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Brumbaugh, Graves, Donohue & Raymond
30 Rockefeller Plaza
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Czegledy, Ferenc
Iserovich, Pavel
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25.2%;
                                                                                             US/08/355,844
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                                                                                                                                                           Version
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RESULT 12 US-09-610-417-5

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                                                                                                            RESULT 14
PCT-US95-16126-3
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Best Local Similarity
                                                                            Sequence 3, Application PC/TUS9516126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-408-2586
TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Tang, Henry Y.S.
REGISTRATION NUMBER: 29,705
REFERENCE/DOCKET NUMBER: A2'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,408-2586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                 APPLICANT:
                                                              APPLICANT:
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                                 APPLICANT:
     APPLICANT:
                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                         424 --FLSIGLYMLGKFGITSAFS-----MLYVFTAELYPTLVRNMAVGYTSTASRVGS-IIA 475
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                                                                                                                                                                          474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGESILPTTLTTLWS-----LSVAIFSVGGMIGSFSVGLFVNRFGRRNSMLMMNL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFATMAVQTGFSFLQIFSISWEM------FTVLFVIVGMGQISNYVVAFILGT 219
                                                                                                                                                                                                                                                                                                                                                                 QQPVYATIGSGIVNTAFTVVSLFVVERAGRRTLHLIGLAGMAGQAILMTIALALLEQLPW 363
                                                                                                                                                                                                                                                                                                                                                                                            EIPAYIT-----AWLLLRTLPRR--YIIAAVLFWGGGVLLFIQLVPVDYY-- 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFILDLFRTRN-----IAIMTIMSLLLWMLTSVGYFALSLDAPNLHGDAYLNCFLSALI 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EILGKSVRIIFSTLGVCTFFAVGYMLLPLFAYFI----RD-WRMLLLALTVPGVLCVPLW 274
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                                                                                                                                                                                                                                                                                                   MSYLSIVAI----FGFVAFFEVGPGPIPWFTVAELESQGPRPAAIAVAGFSNWTSNFIVG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFCPESPRFLLINRNEENRAKSVLK--KLRGTA-----DVTHDLQEMKEESRQMMREKK 256
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linear
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Li, Jun
Cheung, Min
                                                 Czegledy, Ferenc
                                                              Fischbarg, Jorge
                Iserovich, Pavel
Li, Jun
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24.0%;
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Pred. No. 1e-14;
4; Mismatches 1
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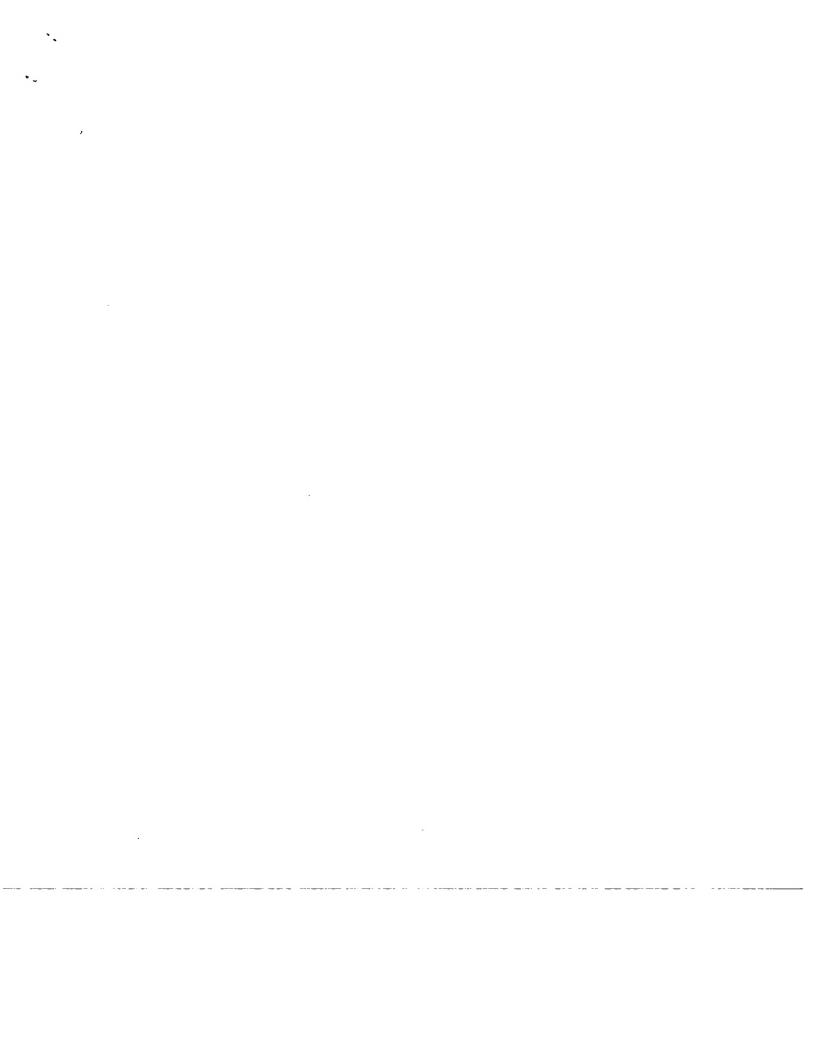
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PCT-US95-16126-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.8%;
Best Local Similarity 24.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08,
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Tang, Henry Y.S.
REGISTRATION NUMBER: 29,70
REFERENCE/DOCKET NUMBER: F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide LOCATION: 1..492 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 FSQDVYLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQLSDRFGRK-----NV 172
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 10112-0228
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CITY: New York
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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QQPVYATIGSGIVNTAFTVVSLFVVERAGRRTLHLIGLAGMAGQAILMTIALALLEQLPW
                                EIPAYIT-----AWLLLRTLPRR--YIIAAVLFWGGGVLLFIQLVPVDYY-- 423
                                                                                                                                                         PFCPESPRFLLINRNEENRAKSVLK--KLRGTA-----DVTHDLQEMKEESRQMMREKK 256
                                                                                                                                                                                                   WFIPESPRWLISQRRFREAEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQQ-----K 326
                                                                                                                                                                                                                                          -----LHQLGI----VVGILIAQVFGLDSIMGNKDLWPLLLSIIFIPALLQCIVI 204
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                                                                                                                                                                                                                                                                                                                                                                 LFATMAVQTGFSFLQIFSISWEM------FTVLFVIVGMGQISNYVVAFILGT 219
                                                                          VTILELFRSPAYROPILIAVVLQLSQQLSGINAVFYYSTSI
                                                                                                                  AFILDLFRTRN-----IAIMTIMSLLLWMLTSVGYFALSLDAPNLHGDAYLNCFLSALI 380
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30 Rockefeller Plaza
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linear
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Pred. No. 1e-14;
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Sequence 10, App....
Sequence 10, App....
Patent No. 5942398
Patent IN INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
ONRESPONDENCES: 10
CORRESPONDENCES ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
TREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                   TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
CHENCYH: 493 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
HOLECULE TYPE: protein
US-09-031-392-10
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US-09-031-392-10
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                                                                                                                                                                                                                       Query Match 7.6%; Score 216; DB 2; Length 493; Best Local Similarity 24.2%; Pred. No. 4.4e-14; Matches 111; Conservative 78; Mismatches 171; Indels
                                                                                                                                                                            144 LTTSLFFVGVLLGSFVSGQLSDRFGRKNVLFA--TMAVQTGFSF-LQIFSISWEMFTVLF 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 QSDKTPEE 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 MCFQYVEQLCGPYVFIIFTVLLVLFFIRTYFKVPETKGRTFDEI-----ASGFRQCGAS 473
                                186 L------WPLILGUTGVPALLQLLLLPFCPESPRYLLINKNEEARAKKALQRLRGTA 236
                                                                                             128 FIIGLYCGLSSGVVPMYVGEISPTALRGALGTLNQLGIVIGILIAQVLGLDSL--LGNES 185
                                                                                                                        476 PYFVYLGAYNRMLPYIVMGSLTVLIGIFTLF-FPESLGMTLPETLEQMQKVKWFRSGKKT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 MSYLSIVAI----FGFVAFFEVGPGPIPWFIVAELESQGPRPAAIAVAGFSNWTSNFIVG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 --FLSIGLVMLGKEGITSAFS-----MLYVFTAELYPTLVRNMAVGVTSTASRVGS-IIA 475
 295 DIIQKAAKMUNTAVPAVIFDSVEELNPLKQQKAFILDLFRTRN----
                                                            246 LPLFAYFIRDWRMLLLALTVPGVLCVPLWWFIPESPRWLI------SQRRFREAE 294
                                                                                                                                                           68 LSVSIFAVGGMIGSFLVGXIGNRLGRKXAMLVNNVLATAGGLLMGLAKXAXSFEMLILGR 127
 --IAIMTIMSLLL 348
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                                                                  391 IVAELESQGPRPAAIAVAGESNWTSNFIVGLLEQYIAELLGPYVFIVFAVLLLLEFIFTF 450
                                                                                                                                                                                                                                                                  FTAELYPTLVRNMAVGVTSTASRVGS-IIAPYFVYLGAYNRMLPYIVMGSLTVLIGIFT- 504
                                                                                                                                  GRTTLHLIGLGGMAGCAVLMTIALALLDQVPWMSYVSIVAI--EGEVAPFEVGPGPIPWF 390
                                                                                                                                                                                                 SGINAVEYYSTSI------FEKAGVGQPVYATIGAGVVNTVFTVVSVFVVERA 332
                                                                                                                                                                                                                                  WMLTSVGYFALSLDAPNLHGDAYLNCFLSALIEIPAYIT------AWLLLRTL 395
LKVPETKGRTFDEIAAAFRKXN--KXEQPEKESIEELE 486
                                LFFPESLGMTLPETLEQMQKVKWFRSGKKTRDSMETEE 542
                                                                                                                                                                  PRR--YIIAAVLFWGGGVLLFIQLVPVDY--YFLSIGLVMLGKFGITSAFS-----MLYV 446
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Search completed: July 17, 2002, 02:03:56 Job time: 5772 sec



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution. printed,

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	5	4	ω	2	1	1 20.	Result
0.67	293.5	294.5	305	307	311	312	312.5	317	317.5	318	318	327	338	356	382.5	393	412.5	421.5	475	484.5	488	548	565	681.5	699.5	754.5	2152	2218	SCOTE	
10.2	10.3	10.4	10.7	10.8	10.9	11.0	11.0	11.1	11.2	11.2	11.2	11.5		12.5	13.4	13.8	14.5	14.8	16.7	17.0	17.2	19.3	19.9	24.0	24.6	26.5	75.6	78.0	масси венуси	Query
400	452	529	461	435	591	450	510	455	1222	437	437	454	540	528	515	751	521	518	539	527	447	745	794	556	593	576	557	557		
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C69/57	AD0300	T23190	AE3208	T15290	T30895	F95360	в88381	в83213	C88504	AB2854	G97630	F75580	T25851	T21682	в96825	C88485	н86298	в86299	C96758	T01019	D89646	T16565	T27870	S50862	JC4884	T22509	JE0346	JW0089		5
transporter nomoto	probable transport	hypothetical prote	MFS permease [impo	hypothetical prote	sugar transport pr	probable transmemb	protein T22F7.1 [i	probable MFS trans	protein B0361.3 [i	MFS permease [impo	probable sugar tra	probable sugar tra			hypothetical prote	protein F23F12.5 [hypothetical prote	hypothetical prote	probablle protein	transport protein	protein ZK455.8 [i	pro	hypothetical prote	organic cation tra	organic cation tra	hypothetical prote	high-affinity carn	organic cation tra	הפאלר ד לי דירו	7000

ALIGNMENTS

JW0089

organic cation transporter protein 2 - human N; Alternate names: OCTN2 (Man) (C.Species: Homo saplens (Man) (C.Species: Name of the same of the sa A;Molecule type: mRNA A;Rosidues: 1-557 <MUA> A;Residues: 1-557 <MUA> A;Cross-references: GB:AF057164; NID:g3273740; PIDN:AAC24828.1; PID:g3273741 A;Experimental source: placenta C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions in the elimination of cationic drugs and C;Comment: This transporter functions are cated as the categories and categories and categories are categories are categories and categories are categories a 밁 Ω 밁 Qy QУ DЬ QΥ 80 망 δÃ В QΥ DЬ В Query Match 78.0%; Best Local Similarity 75.9%; Matches 423; Conservative 5 241 VGYMILPLFAYFIRDWRMLLLALITVPGVLCVPLWWFIPESPRWLISQRRFREAEDIIQKA 300 | ||:|:||||||||||:||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:| 121 419 361 301 301 181 181 TGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLGVCTFFA 240 121 QDVYLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQ 180 61 AWRNHTVPLRLRDGREVPHSCRRYRLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFS 120 61 AKMNNTAVPAVIFD--SVEELNPLKQOKAFILDLFRTRNIAIMTIMSLLLMMLTSVGYFA 358 AWRNNSVPLRLRDGREVPHSCSRYRLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFS 120 AKANGIVVPSTIFDPSELQDLSSKKQQSHNILDLLRTWNIRMVTIMSIMLWMTISVGYFG TGFSFLQIFSKNFEMFVVLFVLVGMGQISNYVAAFVLGTEILGKSVRIIFSTLGVCIFYA QDVYLSTIVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRKNVLFVTMGMQ PVDYYFLSIGLVMLGKFGITSAFSMLYVFTAELYPTLVRNMAVGVTSTASRVGSIIAPYF 478 ; Score 2218; DB 2; ; Pred. No. 1.7e-155; 57; Mismatches 71; Length 557; Indels 6; Gaps drugs and other 360 180 240 ω OCTN2

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RESULT 2
JE0346
high-affinity carntine transporter, CT1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Ccession: JE0346
C;Accession: JE0346
R;Sekine, T; Kusuhara, H.; Utsunomiya-Tate, N.; Tsuda, M.; Sugiyama, Y.; Kanai, Y.; En
Biochem. Biophys. Res. Commun. 251, 586-591, 1998
A;Title: Molecular cloning and characterization of high-affinity carnitine transporter
A;Reference number: JE0346; MUID:99011422
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A; Residues: 1-557 <SEK>
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                                                                                  VYLGAYDRFLPYILMGSLTILTAILTLFFPESFGAPLPDTIDQMLRVKGIKQWQIQSQTR
                                                                                                   VYLGAYNRMLPYIVMGSLTVLIGIFTLFFPESLGMTLPETLEQMQKVKWFRSGK---KTR
                                                                                                                                                PSELFYLSTALVMVGKFGITSAYSMVYVYTAELYPTVVRNMGVGVSSTASRLGSILSPYF
                                                                                                                                                                                                            LSLDAPNIHGDAYINCFISALIEIPAYITAWILLIRTIPRRYIIAAVIFWGGGVLLFIQLV 418
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73.1%;
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Pred. No. 1.2e-150;
8; Mismatches 76;
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organic cation transporter protein 2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1996 #sequence_revision 18-
C;Accession: JC4884
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A;Map position: 1
A;Introns: 16/1; 23/3; 50/1; 80/3; 108/2; 134/3; 221/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F52F12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-576 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T22509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: Z19573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: T
R; Matthews, L.
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T22509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: Z83228; PIDN: CAB05732.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.5%; S
Best Local Similarity 30.2%; P
Matches 169; Conservative 119;
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                                                                                                                                                                                                                                                                                                                                         VGYFALSLDAPNLHGDAYLNCFLSALIEIPAYITAWLLLRTLPRRYITAAVLFWGGGVLL 413
                                                                                                                             PEPDSGMFTQAAKKRESQP
                                                                                                                                                                                                                                                                          FIQLVPVDYYFLSIGLVMLGKFGITSAFSMLYVFTAELYPTLVRNMAVGVTSTASRVGSI 473
                                                                                                                                                                                                                                                                                                                                                                                                       KMN---NTAVPAVIFDSVEELNPLKQQKAF----ILDLFRTRNIAIMTIMSLLLWMLTS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMALLGVVAMFIRRWRQLTFFCNAPFAFYIIYYFFLPESPRWSVSVGKWADAKKQLKKIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVYLSTVYTEWNLVCEDNWKYPLTTSLFFYGYLLGSFYSGQLSDRFGRKNVLFATMAYQT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTNDTQIL-----
                                                                                                                                                                                          LAPHIVNLGKIVKILPLLIMGLMALSAGILTFFLPETLGAPLPMTIEDAENF---
                                                                                                                                                                                                                     IAPYFVYLGAYNRMLPYIVMGSLTVLIGIFTLFFPESLGMTLPETLEQMQKVKWFRSGKK 533
                                                                                                                                                                                                                                                        SAMEMPDGYPWLVASASFIGKEGVGSGFAVIYIFAGELYPTVVRAIGMGMSSMVAGSGLL 482
                                                                                                                                                                                                                                                                                                                      IIYNGLTLNVSNLPVDDYWSFIINGAVELPGYFVVWPLLQCAGRRWTLAATMIVCGIGCV 422
                                                                                                                                                                                                                                                                                                                                                                                  KMNGKSNVDVDELV-DSMKNHQNAAEEKETKRSHNVTDLFKTPNLRRKTLIVTYIWVMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYMLLPLFAYFIRDWRMLLLALTVPGVLCVPLWWFIPESPRWLISQRRFREAEDIIQKAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCGTASSFAKDIESFIILRFFTGLAFPALFQIPFIICMEFMGNSGR-IFSGLMTSLFFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLGVCTFFAV 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFDFVLEQVGNYGTYQIVFFFIICLPTSLPSAFSAFNIPFVVGNPPHTCHIPEGKEYLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYDEVIAFLGEWGPFQRLIFFLLS-ASIIPNGFNGMSVVFLAGTPEHRCRVPDAANLSSA 61
                                                                                                                                                            -TRDSMETEENP
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                                                                                                                             556
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Pred. No. 7.2e
L9; Mismatches
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           18-Oct-1996 #text_change
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nes 236;
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05-Nov-1999

537

362

303

243

DB

2;

257/2;

319/3; 358/2; 490/3; 5

Indels Length

35;

Gaps

9

GSPDB:GN00019;

CESP: F52F12.1

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organic cation transport protein OCT1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Nov-1999
C:Accession: $50862; $79533; IS8089
R:Gruendemann, D.; Gorboulev, V.; Gambaryan, S.; Veyhl, M.; Koepsell, H.
Nature 372, 549-552, 1994
A:Pitle: Drug excretion mediated by a new prototype of polyspecific transpor A; Reference number: IS8089; MUID:95082907
A; Rocession: $50862
A; Molecule type: mRNA
A; Residues: 1-556 <GRU>
A; Rosidues: 1-556 <GRU>
A; Experimental source: Kidney
R; Gorboulev, V.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Okuda, M.; Saito, H.; Urakami, Y.; Takano, M.; Inui, K.
Blochem. Blophys. Res. Commun. 224, 500-507, 1996
A;Title: CDNA clonning and functional expression of a novel rat kidney organic A;Reference number: JC4884; MUID:9629517
A;Accession: JC4884
A;Mclecule type: mRNA
A;Residues: 1-593 <OKU>
A;Cross-references: DDBJ:D83044; NID:g1502282; PIDN:BAA11754.1; PID:d1012421; A;Experimental source: kidney
C;Comment: This protein is responsible for the transport of cationic drugs in
                                                                                                                                                                                                                                                                                                   RESULT
S50862
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRNQLPLGPCEHGWYYNTPG--SSIVTEFNLVCAHSWMLDLFQSVVNVGFFIGAMMIGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRDYDEVIAFLGEWGPFQRLIFELLSASIIPNGFNG--MSVVFLAGTPEHRCRVPDAANL
                                                                                                                                                                                                                                                                                                                                                                                           EDAENMQ - - RPRKKER
                                                                                                                                                                                                                                                                                                                                                                                                                                  EQMQKVKWFRSGKKTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLVCSSMCDIGGIITPFLVYRLTDIWMEFPLVVFAVVGLVAGALVLLLPETKGKALPETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGVTSTASRVGSIIAPYFVY-LGAYNRMLPYIVMGSLTVLIGIFTLFFPESLGMTLPETL 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAAVLFWGGGVLLFIQLVPVDYYFLSIGLVMLGKFGITSAFSMLYVFTAELYPTLVRNMA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLILMYNWFTSSVLYQGLIMHM-GLAGDNIYLDFFYSALVEFPAAFIIILTIDRVGRRYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIMSLLLWMLTSVGYFALSLDAPNLHGD-AYLNCFLSALIEIPAYITAWLLLRTLPRRYI 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RWLISONKIVKAMKIIKHIAKKNGKSVPVSLONLTPDEDAGKKLKPSILDLVRTPQIRKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGYR---RMVGICYQIAFTVGLLILAGVAYVIPNWRWLQFAVTLPNFCFLLYFWCIPESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSVRIIFSTLGVC--TFFAVGYMLLPLFAYFIRDWRMLLLALTVPGVLCVPLWWFIPESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADRFGRKFCLLVTILINAISGALMAISPNYAWMLVFRFLQGLVSKAGWLIGYILITEFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLGQLEQESCLDGWEFSQDVYLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQRCGWSQAEELNYTVPGLGPSDEASFLSQCMRYEVDWNQSTLDCVDPLSSLA-----A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSTVDDILEHIGEFHLFQKQTFFLL--ALLSGAFTPIYVGIVFLGFTPDHHCWSPGAAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WAVSNMVAGAACLASVFIPDDLQWLKITIACLGRMGITMAYEMVCLVNAELYPTYIRNLG
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F:20-46/Domain: transmembrane #status predicted <TM1>
F:154-171/Domain: transmembrane #status predicted <TM2>
F:178-197/Domain: transmembrane #status predicted <TM3>
F:243-260/Domain: transmembrane #status predicted <TM4>
F:267-283/Domain: transmembrane #status predicted <TM5>
F:267-283/Domain: transmembrane #status predicted <TM5>
F:350-366/Domain: transmembrane #status predicted <TM7>
F:380-398/Domain: transmembrane #status predicted <TM8>
F:406-425/Domain: transmembrane #status predicted <TM8>
F:405-425/Domain: transmembrane #status predicted <TM10>
F:469-485/Domain: transmembrane #status predicted <TM10>
F:469-485/Domain: transmembrane #status predicted <TM10>
F:494-514/Domain: transmembrane #status predicted <TM10>
F:494-514/Domain: transmembrane #status predicted <TM10>
F:494-514/Domain: transmembrane #status predicted <TM10>
F:495-350/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted <TM10-
F:286,392/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted <TM10-
F:296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted <TM10-
F:296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted <TM10-
F:296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted <TM10-
F:296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted <TM10-
F:296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted <TM10-
F:296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted <TM10-
F:296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted <TM10-
F:296,343,550/Binding site: phosphate (Thr)
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C;Keywords: glycoprotein; phosphoprotein; transmembrane
F;20-46/Domain: transmembrane #status predicted <TM1>
F;154-171/Domain: transmembrane #status predicted <TM3>
F;178-197/Domain: transmembrane #status predicted <TM3>
F;243-260/Domain: transmembrane #status predicted <TM4>
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A; Reference number: $78533
A; Accession: $78533
A; Molecule type: mRNA
A; Residues: 1-342,'N',344-556
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                                                    511 LGMTLPETLEQMQKV 525
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                                                                                                                                                                                YPTLVRNMAVGVTSTASRVGSIIAPYFVY-LGAYNRMLPYIVMGSLTVLIGIFTLFFPES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILGTEILGKSVR----IIFSTLGVCTFFAVGYMLLPLFAYFIRDWRMLLLALTVPGVLCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPTVDDVLEQVGEFGWFQKQAFLLLCLISASLAP---IYVGIVFLGFTPGHYCQNPGVAE
                                                                                                                                                                                                                                               IDRIGRIYPIAASNLVTGAACLLMIFIPHELHWLNVTLACLGRMGATIVLQMVCLVNAEL
                                                                                                                                                                                                                                                                                                      LRTLPRRYITAAVLFWGGGVLLFIQLVPVDYYFLSIGLVMLGKFGITSAFSMLYVFTAEL 451
                                                                                                                                                                                                                                                                                                                                                                     LFRTPTLRKHTVILMYLWFSCAVLYQGLIMHVGATGANLYLDFFYSSLVEFPAAFIILVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSS--AWR----ATIANFSAL
   KGVALPETIEEAENL
                                                                                                                  YPTFIRNLGMMYCSALCDLGGIFTPFMYFRLMEVWQALPLILFGYLGLTAGAMTLLLPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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33.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 681.5;
Pred. No. 1.6e
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6e-42;
ches 231;
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hypothetical protein ZK455.8 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t

15-Oct-1999 #text_change

18-Feb-2000

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C; Accession: T27870
R; White, S.
submitted to the EMBL Data Library,
A; Reference number: Z20432
A; Accession: T27870
hypothetical protein K05F1.6 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #te C:Accession: T16565 #Sequence_revision 20-Sep-1999 #te C:Accession: T16565 R;Wohldmann, P. submitted to the EMBL Data Library, June 1995 submitted to the EMBL Data Library, June 1995 A;Description: The sequence of C. elegans cosmid K05F1 A;Reference number: Z18537 A;Accession: T16565 A;Status: preliminary; translated from GB/EMBL/DDBJ
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T16565
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A; Introns: 52/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z66567; PIDN:CAA91492.2; GSPDB:GN00028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFEEDDLGILQLIGGCSYWQIIVYLIISVQQVPHAMFNLSVVYMMYQPDHWCKIPFFNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYDE----VIAFLGEWGPFQRLIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVP----
                                                                                                                                                                                                                                                                                                               QLSDRFGRKNVLFATMAVQTGFSFLQIFSISWEMFTVL-FVIVGMGQISNYVVAFILGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----DAANLSSAW---RNNSV--PLRLRDGREVPH--SCSRYRLATIANFSALGLEPGRD
                                                                                                                                                                                                                                                                  VGSIIAPYFVYLGAYNR-MLPYIVMGSLTVLIGIFTLFFPESLGMTLPET-LEQMQKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTGTKYRSIVGSL-IQAPWACGYAFLALIAYLTKSWTMIHLICVLLHIISLMLLYFLPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISDRYGRKTAITGFGILTMLFGFLLTYSKEFEIFLVVRFLLAATNEAAD-LAAYVLCME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKDMNATGKINRCKEWEYDTSVMDRTIVTEWNRVCDNNWSRAHVHMSYSLGYLVGCFVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFSAELGYTNYTWDQVLNSTIAFPRTFNKQRNELHHDQCHYFE----RDYVHIKLSPWAQ
                                                                                                                                                                                                                                              MGAGASGYIAILSDVTMPLVPMTIFACFSLLAGCLVLLLPETQGLPLPDTILDSVQMVK
                                                                                                                                                                                                                                                                                                                                                LLFIQLVPV--DYYFLSIGLVMLGKFGITSAFSMLYVFTAELYPTLVRNMAVGVTSTASR
                                                                                                                                                                                                                                                                                                                                                                                  NQKLCFRRVFD-----GNFFLNNAMAGAIELPTLVFCVFLLR-MGRKRSQMLVLF-GSGL
                                                                                                                                                                                                                                                                                                                                                                                                      ----FALSLDAPNLHGDAYLNCFLSALIEIPAYITAWLLLRTLPRRYIIAAVLFWGGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRFRNVVLFIVWVIQKNIFQNSRFQYSDSNCSGLLRNGYCIVRSVITRKVGRTLSEKFYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRWLISQRRFREAEDIIQKAAKMNNTAVPA--VIFDSVEELNPLK-QQKAFILDLFRTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILGKSVRIIFSTLGVCTFFAVGYMLLPLFAYFIRDWRMLLLALTVPGVLCVPLWWFIPES
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26.48;
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Pred. No. 8.9e-34
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                                                         K05F1
                                                                                                                          #text_change
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Qy

Qy 밁 20 В

밁 δÃ Вb

A; Cross-references: GB:chr_X; PIDN:CAA91492.1; A; Note: Similarity to sugar transporters

PID: 93881642;

GSPDB:GN00028;

CESP: ZK45

A; Note: Sim C; Genetics:

QΥ 밁 γ В 8 В δÃ Вb 20 В QΥ

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A; Molecule type: DNA
A; Residues: 1-745 <WOH>
A; Cross-references: EMBL: U29377; NID: 9868173;
A; Experimental source: strain Bristol N2
C; Genetics: C754
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A; Introns: 70/2; 160/3;
                                                                                  R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a particle: A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and A;Note: published errata appeared in Science 283, 35, 19
                                                                                                                                                                                                                          protein ZK455.8 [imported] - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 10-May-2001 #sequence_revision 10-May-2001
A; Molecule type: DNA
A; Residues: 1-447 <STO>
                                                          A;Note: published errata appeared A;Accession: D89646
                                                                                                                                                                                                           C; Accession:
                                      A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAFILGTEILGKSVRIIFSTLGVCTFFAVGYMLLPLFAYFIRDWRMLLKALTVPGVLCVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAMSEAWKDV----APKKKC-QAYHFEKDVMVETIVTDFNLVC-DSWFAKGHAHMFYSIG
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                                                                                                                                                                                                                                                                                                                                                                           PIVPM---
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                                                                                    and www_sanger.ac.uk/Projects/C_
, 1999; Science 283, 2103, 1999;
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C;Genetics:
A;Gene: ATSI
A;Map posit:
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TO1019
transport protein homolog YUP8H12R.2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change
C;Accession: T01019
C;Accession: T01019
                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A;Description: Arabidopsis thaliana A;Reference number: Z14227 A;Accession: T01019
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A; Map position:
                                                                                                                                                                                                                                                       A;Cross-references: EMBL;AC002986; NID:g2494106; PID:g3152576; GSPDB:GN00059; ATSP:YUP81A;Experimental source: cultivar Columbia
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A; Residues: 1-527 <THE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 LALIAYLTKSWTMIHLICVLLHIISLMLLYFLPESPRWLILNNKTKQAEKIIREACHYNK 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LTYSKEFEIFLVVRFLLAATNEAAD-LAAYVLCMEVTGTKYRSIVGSL-IQAPWACGYAF
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                                                                                                                                                                                                                   ATSP:YUP8H12R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGITSAFSMLYVFTAELYPTLVRNMAVGVTSTASRVGSIIAPYFVYLGAYNR-MLPYIVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRLPSDLGLVRHAEKKKWMKHNEKPSYFHLFRSSELRFRNVVLFIVWVIQKNIFQNSRFQ
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 AWRNNSVPLRLRDGREVPHSCSRYRLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFS
                                   RSLDDTIESYIGSFGWAQFLQAALVSFSGVFDAQQTFISVFTDSEPTWHC------
                                                                    RDYDEVI-AFLGEWGPFQRLIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVPDAANLSS
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                                                                                                           Conservative
                                                                                                       17.0%; Score 484.5; DB 2; 27.0%; Pred. No. 4.7e-28; tive 99; Mismatches 209;
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Pred. No. 2.1e-28;
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chromosome 1 YAC
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                FPESLGMTLPETLEQ 521
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LPETRGSDLCDTMDE
                                                                                                                                                                                                                                                         SILKRVASIPSTDVSSGGAISMSFSSLPFEEDEEKP--
                                                                                                                                                                                                                                                                                                                                       QTGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLGVCTFF
                                                              YTIELFPTCVRNSAIAMARQALVLGGVFSPIMVAAGRKNAFWSFGLFGLAIGLLGLFAVG
                                                                                            FTAELYPTLVRNMAVGVTSTASRVGSIIAPYFVYLGAYNRMLPYIVMGSLTVLIGIFTLF
                                                                                                                             LVDKLSRRNALIGFTALGGVSSVLIFALHNMRIGNHGALQLALELISYFSACSAFNMEMI
                                                                                                                                                         LLRTLPRRYIIAAVLFWGG--GVLLFI--QLVPVDYYFLSIGLVMLGKFGITSAFSMLYV 446
                                                                                                                                                                                          VLVEKRWALKRLSAVMAIAFGIGLVYYGMPLALSNLDFNIYLSAAFNALMDLPANLITLF
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, Y.H.; Lin, Y.; Lin, S.X; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719 A; Molecule type: DNA A; Residues: 1-539 <STO> A; Cross-references: GB: probablle protein transporter T18K17.11 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96758 Qy Дδ Qy DЪ A; Map position: C; Genetics: A; Gene: T18K17.11 A; Status: preliminary Query Match Best Local 138 144 LTTSLFFVGVLLGSFVSGQLSDR-FGRKNVLFATMAVQTGFSFLQIFSISWE-----97 87 10 VPSTLFFIGSLFGSGVYGYLADSWFGRKKTLLLSCVL----TEVTAFAISFSPNVWVYAF AIVEGASLCGLASGE----ATIANFSALGLEPGRDVDLGQLEQESCLDGWEF - - - SQDVYLSTVVTEWNLVCEDNWKVP 143 al Similarity 145; Conserv Conservative GB:AE005173; 16.7%; Score 475; DB 2; 29.8%; Pred. No. 2.4e-27; tive 82; Mismatches 193 NID: g6598860; WEWIGPKSD----TVVSEWNLICQHKFLVA 137 PIDN:AAF18714.1; GSPDB:GN00141 193; Length 539 Indels 66; Gaps 193 194 13;

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wł Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A; Residues: 1-518 <ST
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A;Accession: B86299
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                                                                                                                                                                                             RDYDEVI-AFLGEWGPFQRLIFFLLSASIIPNGFNGMSVVFLAGTPEHRC----RVPDAA
TMAVQTGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLGV
                                                            WEFSQDVYLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQLSD-RFGRKNVLFA 175
                                                                                                                                                             {\tt RSLEETIERCIGDFGWAQFLQAALVSFAWFFDAQQTFITVFTDSQPMWHCDNSDRVDSVC}
                                WSWDLNPHVS-IISEWGLQCAGSFLKGFPASSFFLGCLIGGLALSTLADSSLGRKNMLLL
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138; Conserv
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                                                                                                                                                                                                                                                                                                                                           GB:AE005172;
                                                                                                                                                                                                                                             14.8%;
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Pred. No. 2e-23;
90; Mismatches 233;
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Maiti, R.; M
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A; Residues: 1-521 <S
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504 DE
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EAIDVLTKMSPKEK
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hypothetical protein F309.17 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: H86298
R:Pheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O., Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; P., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; P., Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEFSQDVYLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQL-SDRFGRKN-VLF 174
                                                                                                                                                                                      VCTFFAVGYMLLPLFAYFIRD--WRMLLLALTVPGVL-CVPLWWFIPESPRWLISQRRFR
                                                                          EAEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQQ-----
                                                                                                                                                 PFTLFVLGFMSLSGIAFLAQDSSWRYLYLYTSVPAVFYCIFLYLFALESPRWLHMQGKDK 275
                                                                                                                                                                                                                                                                                           STFAMSI-TSISVIFSTNVWIYTFLKFIIGFSRSQTWSYALVLISERVSTRWR-PRATMI 215
                                                                                                                                                                                                                                                                                                                                                          ATMAVQTGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLG 234
                                                                                                                                                                                                                                                                                                                                                                                                                             WEWDGGSQGKSVISEFGLECSSSLLRGMPSSAFYIGAIVGGFFLALIPpDSLGRKKLVLF 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCLIMSLSSMLTAFSTSIWVYAFLRFLNGCGRATIGTCALVLSTELVGKKWR---GQVGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:AE005172; NID:g4966358; PIDN:AAD34689.1; GSPDB:GN00141
-AYLESVVSKLPLKQENFEQAPTYSIKDFFFRKWAFRRILVV 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 412.5; DB 2
Pred. No. 9.1e-23;
1; Mismatches 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                          ---KAFILDLFRTRNIAIM 341
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Maiti, R
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Tallo

Kim,

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protein F23F12.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C88A85
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99059613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: C88485
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A; Molecule type: DNA
A; Residues: 1-751 <STO>
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 TAELYPTLVRNMAVGVTSTASRVGSIIAPYFVYLGAYNRMLPYIVMGSLTVLIGIFTLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342
                                                                                                                                                                                                                                                                                                                     478
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                                                                                                                                                                                407
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                                                                                                                                                                                                                                                                                                                                                         NNTAVPAV-----IFDSVEELNPLKQQKAFIL-DLFRTRNIAIMTIMSLLLWMLTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLGVCTFFAVGY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETKGLSLCDSMEEQEK 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PESLGMTLPETLEQMQK 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAVLFWGG ~ - GVLLFIQLVPVDYYFLSIGLVMLGKFGITSA - - - - - - - ESMLYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIIMFGL----GISYYGVPLAARDIDVNIYLSETLNALVELPTFVITPILLERFNRRSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIMSLLLWMLTSVGYFALSLDAPNLHGDAYLNCFLSALIEIPAYITAWLLLRTLPRRYII
                                                                                                                                                                                                                        SAFGSDLNSGNLAGNFYLSQFVSGAVTAFAKIFVFLLDTYVPSFDRRRLHQYPQIAMILC
                                                                                                                                                                                                                                                                   GYFALSLDAPNLHGDAYLNCFLSALIEIPAYITAWLLLRTLP---RRYI----IAAVLF 406
                                                                                                                                                                                                                                                                                                                --SGIPYVNDEDQSIEISEKLEE----KSTKIYTMKDLFTSWTIAYRTIVVGSLWFSTSL
                                                                                                                                                                                                                                                                                                                                                                                                      LVFTLACFICGYWRSAAIATSLLSLPILPVLLILPESPKWFNTKKRFRDARAAEKRVAWL
                                                                                                                                                                                                                                                                                                                                                                                                                                               MLLPLFAYFIRDWRMLLLALTVPGVLCVPLWWFIPESPRWLISQRRFREAEDIIQKAAKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMVQDFKMFCGTKAYDAAWVATIQFIGVLIGAITYGHLGDHFGRKPVSFFGISVGILFGV
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                                                                                     NMAVGVTSTASRVGSIIAPYFVYLGAYNRMLPYIVMGSL-TVLIGIFTLEEPESLGMTLP 516
                                                                                                                                   Y -- CVIMVLMILPESDCGSQGSRDLAIIIINIIGVSFIEIT -- WDACYLVAVECFPTKIR
                                                                                                                                                                           WGGGVLLFIQLVPV------DYYFLSIGLVMLGKFGITSAFSMLYVFTAELYPTLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
119; Conserv
    ETLEOMOKVKWFRSGKKTRD 536
                                             TIGIGTCSLLARTGALLAPQMAYLSDIYRPAPYAVVCSIGTISLLISCVFLPDTKGVDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.8%; score 393; DB 2; Length 751; 27.0%; Pred. No. 3.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:AAA20607.1; PID:g529214; GSPDB:GN00021; CESP:F23F1
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                                             706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
hypothetical protein F32H5.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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RESULT

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.F.; Li, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B96825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T8K14.17 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar_2001 #sequence_revision 02-Mar_2001 #text_change 31-Mar-2001
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C;Genetics:
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A; Residues: 1-515 <STO>
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                                                                                                                                          434
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474
                                             494
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                                          GSLTVLIGIFTLFFPESLGMTLPETLEQMQK 524
                                                                                                                                                                                        LPTFYVTPILLEQFSRRSSVLVNCLIGGASGYLCFVMSL---YGRTKIAFALELGSFFCA 417
                                                                                                                                                                                                                                                                                                                           AF-ILDLE----RTRNIAIMTIMSLLLWMLTSVGYFALSLDAPNLHGDAYLNCFLSALIE
                                                                                                                                                                                                                                                                                                                                                                           SIFIYFFALESPRWLHLEGKNKEAIEVLKRISPANRGYLESV----SSRLRPKETLEQTS
                                                                                                                                                                                                                                                                                                                                                                                                      CVPLWWFIPESPRWLISQRRFREAEDIIQKAAKMNNTAVPAVIFDSVEELNP---LKQQK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGVVLAMIPDGSLGRKQLLFFSSFAMSLTGISIF-LSSNIW-IYSFLKFVIGFARSQTGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSFVSGQLSD-RFGRKNVL-FATMAVQ-TGFSFLQIFSISWEMFTVLFVIVGMGQISNYV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLDHTICNPATTDICKIPRSAWDWDGGFKGKSVISEFDLECSSSFLRSLPSSTFYVGSIV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AALDPTEELDYDRKKSMTEN
                                                                                                                                        KFGITSAFSMLYVFTAELYPTLVRNMAVGVTSTASRVGSIIAPYFVYLGAYNRMLPYIVM 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAFILGTEILGKSVRIIFSTLGVCTFFAVGYMLLPLFAYFIR--DWRMLLLALTVP-GVL
                                                                                                                                                                                                                                                                                SYSIKDLFIIKWAFRRVTLVMIIMFGLGM----SYYGVPLAVRDIKVNIYMSEALNAMVE
GFAMSGLGLFALLLPETKGLSLCDTMEEQEQ
                                                                                                                                                                                                                                  IPAYITAWLLLRTLPRRYIIAAVLFWGG--GVLLFIQLVPVDY----YFLSIGLVMLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118;
                                                                                          RIG----FNLMAIYLVELFPTCVRNSATMMLRQALVVGGACCPLIASLGRNVPSLSFAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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26.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 382.5; DB 2;
Pred. No. 1.4e-20;
98; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID:g4835768; PIDN:AAD30235.1;
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A;Experimental source: clone F32H5
C;Genetics:
A;Gene: CESP:F32H5.4
A;Map position: 5
A;Introns: 63/1; 108/3; 148/3; 249/2; 408/1; 472/3
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A;Reference number: 219458
A;Accession: T21682
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-528 <WIL>
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R;Steward, C.
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513
                                        522
                                                                             454 FKSSASRIGTILGPQLFILCPY-KSLPYAILTGFCLFDAIAFQLRLPETKGKPLPETMPE 512
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RHK 515
                                                                                                                 VTSTASRVGSIIAPYFVYLGAYNRMLPYIVMGSLTVLIGI-FTLFFPESLGMTLPETLEQ 521
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                                        MQK 524
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                                                                                                                                                                                                      ------VPVDYYF-----LSIGL-VMLGKFGITSAFSMLYVFTAELYPTLVRNMAVG 462
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Search completed: July 17, 2002, 02:05:09 Job time: 1340 sec

OM protein -Run on: protein search, using sw model July 17, 2002, 02:03:59; Search time 39.73 Seconds (without alignments) 536.986 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

ritle:
 perfect score:
 sequence: US-09-521-195B-1 2845

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 MRDYDEVIAFLGEWGPFQRL.....KKTRDSMETEENPKVLITAF 551

Total number of hits satisfying chosen parameters: Searched: 105224 seqs, 38719550 residues

105224

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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VARIANT CDSP GLN-169. WEDLINE-9935597; pubMed-10425211; BUTWINKel B., Kreuder J., Schweitzer S., Vorgerd M., Gempel K., Gerbitz KD., Kilimann M.W.; "Carnitine transporter OCTN2 mutations in systemic primary carnitine deficiency: a novel Argl69Gln mutation and a recurrent Arg282ter	ubMed=9618255; Leibach F. H., Ganapathy V.; nsport function, and genomic organ of the organic cation transporter les. Commun. 246:589-595(1998). ubMed=9685390; Nezu JI., Yabuuchi H., Oku A., litine transporter OCTN2."; 20378-20382(1998). ubMed=9916797; Oku A., Ohashi R., Yabuuchi H., Ha Roizumi A., Shoji Y., Takada G., Chura T., Tsujimoto G., Hayakawa arnitine deficiency is caused by n min ion-dependent carnitine transpor largad P.D., Seth P., Rajan D.P., Le asad P.D., Seth P., Rajan D.P., Le casad P.D., Le casad P.D., Seth P., Rajan D.P., Le casad P.D., Seth P., Rajan D.P., Le casad P.D., Seth P., Rajan D.P., Le casad P.D., Seth	LT 1 HUMAN STANDARD; PRT; 557 AA. OCC2_HUMAN STANDARD; PRT; 557 AA. OCC2_HUMAN STANDARD; PRT; 557 AA. OCC2_HUMAN STANDARD; PRT; 557 AA. OCC2_C2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) Organic cation/carnitine transporter 2 (Solute carrier family 22, member 5) (High-affinity sodium-dependent carnitine cotransporter). SLC2A5 OR OCTN2. SLC2A5 OR OCTN2. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Wang Y., Kelly M.A., Cowan T.M., Longo "A missense mutation in the OCTN2 gene carnitine transport activity.";
Hum. Mutat. 15:238-245(2000).
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                         EMBL; AF057164; AAC24828.1; -.
EMBL; AB015050; BAA29023.1; -.
EMBL; AB016625; BAA36712.1; -.
MIM; 603377; -.
MIM; 212140; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wanders R.J., Fok T.F., Hjelm N.M.;
Wanders R.J., Fok T.F., Hjelm N.M.;
"Mutations of OCTN2, an organic cation/carnitine transporter, lead to the control of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUM.
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Hum. Mol. Genet. 8:655-660(1999).
[8]
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MEDLINE-99172075; Pul
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                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY, SKELETAL MUSC
HEART AND PLACENTA.
DISEASE: DEFECTS IN SLC22A5 ARE THE CAUSE OF SYSTEMIC PRIMARY
CARNITINE DEFICIENCY (COSP). CDSP IS AN AUTOSOMAL RECESSIVE
DISORDER OF FATTY ACID OXIDATION CAUSED BY DEFECTIVE CARNITINE
TRANSPORT. PRESENT EARLY IN LIFE WITH HYPOKETOTIC TYPOGLYCEMIA
ACUTE METABOLIC DECOMPENSATION, OR LATER IN LIFE WITH SKELETAL
MYOPATHY OR CARDIOMYOPATHY.
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. ORGANIC
CATION SUBFAMILY.
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Scholte H.R., Ruiter J., H
Pereira R., Schweitzer S.,
  IPR003662; sub_transporter
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                   LSLDTPNLHGDIFVNCFLSAMVEVPAYVLAWLLLQYLPRRYSMATALF
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75.9%;
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POTENTIAL.
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N-LINKED (GLCNAC.
R-> Q (IN CDSP).
/FTId=VAR_009252.
Y-> C /TW
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E -> K /TM ~~25
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/FTId=VAR_009257.
/FTId=VAR_009257.
M->R: LOSS OF BOTH C
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Pred. No. 2.
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P -> L (IN CDSP;
TRANSPORT BUT STI
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/FTId=VAR_009253
W -> R (IN CDSP)
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V -> F (IN CDSP)
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2.5e-136;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
0rganic cation/carnitine transporter 2 (Solute carrimember 5) (High-affinity sodium-dependent carnitine
                                                         entities
or send a
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the Eurc
         EMBL;
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[2]
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Schoemig E., Spitzenberger F., En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                      cation transporter transporter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and characterization
transporter from rat intestine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sekine T., Kusuhara
Kanai Y., Endou H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SPRAGUE-DAWLEY; TISSUE=Intestine; MEDLINE=99011422; PubMed=9792817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning and characterization proteins from rat kidney."; PEBS Lett. 425:79-86(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen J., Conway S.J., Ganapathy V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99384224; PubMed=10454528; MU X., Huang W., Prasad P.D., Seth P., Rajan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                             Pharmacol. Exp. Ther. 290:1482-1492(1999).
- FUNCTION: SODIUM-ION DEPENDENT, HIGH AFFINITY CARNITINE
TRANSPORTER. ALSO TRANSPORTS ORGANIC CATIONS WITHOUT THE
INVOLVEMENT OF SODIUM. INVOLVED IN THE ACTIVE CELLULAR UPTAKE
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SIMILARITY:
CATION SUBFA
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CORNITINE PROXIMAL AND DISTAL TUBULES AND IN THE GLOMERULI IN THE KIDNEY, IN THE MYCCARDIUM, VALVES, AN ARTERIOLES IN THE HEART, IN THE LABYRINTHINE LAYER OF THE PLACENTA, AND IN THE CORTEX, HIPPOCAMPUS, AND CEREBELLUM IN THE
                                                                                                                               ween the Swiss Institute of Bioinformatics Institute.
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                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way the content in the content is in no way the content is in no way the content in the content is in no way the content in the content in the content is in no way the content in the content 
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AB017260;
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       CAA05106.1;
BAA34399.1;
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                                                                                                                                                                                                                      SUGAR TRANSPORTER FAMILY.
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Murinae; Rat
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RESULT 3
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AC Q9Z0E8;
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Query Match
Best Local S
Matches 408
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Transport;
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Pfam; PF00
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TOKOGGESPTVLKSTAF
                                       VYLGAYDRFLPYILMGSLTILTAILTLFFPESFGAPLPDTIDQMLRVKGIKQWQIQSQTR
                                                  VYLGAYNRMLPYIVMGSLTVLIGIFTLFFPESLGMTLPETLEQMQKVKWFRSGK---KTR
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TE; PS00216; SUGAR_TRANSPORT_1;
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08; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003662; sub_transporter
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233
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342
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73.2%;
                   551
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POTENTIAL.
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POTENTIAL.

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N-LINKED (GLCNAC...

N-LINKED (GLCNAC...

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N-17247227B0A5F043 CF
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POTENTIAL.
POTENTIAL.
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Pred. No. 6.
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.6e-133;
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MEDLINE-99118835; PubMed-9916797;

Nezu J., Tamai I., Oku A., Ohashi R.,

Nikaido H., Sai Y., Koizumi A., Shoji

Yashino M., Kato H., Ohura T., Tsujimo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Chen J., Conway S.J., Ganapathy V.;
"Functional characteristics and tissue distribution
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STRAIN=C3H;
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                                                                                                        Transport;
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FUNCTION: SODIUM-ION DEPENDENT AFFINITY CARNITINE TRANSPORTER. ALSO TRANSPORTS ORGANIC CATIONS WITHOUT THE INVOLVEMENT OF SODIUM. INVOLVED IN THE ACTIVE CELLULAR UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K., Nishimori H., Nakamura Y., Shima K., Kuwajima M., missense mutation of mouse OCTN2, a sodium-dependent transporter, in the juvenile visceral steatosis mouse. ochem. Biophys. Res. Commun. 252:590-594(1998).
                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EMETOPEAN Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content iffied and this statement is not removed. Usage by and itless requires a license agreement (See http://www.isb-send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    CARNITINE.
SUBCELLULAR LOCATION: Integral
DISEASE: DEFECTS IN SLC22A5 ARE
STEATOSIS (JVS).
SIMILARITY: BELONGS TO THE SUGA
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AF111425; AAC99787.1;
AF110417; AAD54060.1;
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00083; sugar_tr; 1.
PS00216; SUGAR_TRANSPORT_1;
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Y., Takada G., Matsuishi
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Rhabditidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLLPLFAYFIRDWRMLLLALTVPGVLCVPLWWFIPESPRWLISQRRFREAEDIIQKAAKM
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          AALDPTEELDYDRKKSMTEN
                                                                       ETLEQMQKVKWFRSGKKTRD
                                                                                                                                                                                                 NMAVGVTSTASRVGSIIAPYFVYLGAYNRMLPYIVMGSL-TVLIGIFTLFFPESLGMTLP
                                                                                                                                                                                                                                                                     Y -- CVIMVLMILPESDCGSQGSRDLAIIIINIIGVSFIEIT -- WDACYLVAVECFPTKIR
                                                                                                                                                                                                                                                                                                                               WGGGVLLFIQLVPV------DYYFLSIGLVMLGKFGITSAFSMLYVFTAELYPTLVR
                                                                                                                                                                                                                                                                                                                                                                                                SAFGSDLNSGNLAGNFYLSQFVSGAVTAFAKIFVFLLDTYVPSFDRRRLHQYPQIAMILC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --SGIPYVNDEDQSIEISEKLEE----KSTKIYTMKDLFTSWTIAYRTIVVGSLWFSTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVFTLACFICGYWRSAAIATSLLSLPILPVLLILPESPKWFNTKKRFRDARAAEKRVAWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMVQDFKMFCGTKAYDAAWVATIQFIGVLIGAITYGHLGDHFGRKPVSFFGISVGILFGV
                                                                                                                                       TIGIGTCSLLARTGALLAPQMAYLSDIYRPAPYAVVCSIGTISLLISCVFLPDTKGVDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
119; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L protein; 4, 5, 7, 7, 7, 7, 7, 102 12, 12, 12, 23, 22, 23, 3, 34, 8, 41, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44, 9, 44
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27.0%;
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Pred. No. 2.4e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184;
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Best Local Similarity
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01-OCT-1996
01-OCT-1996
16-OCT-2001
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 139.9 kDa protein B0361.3 in chr
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Rhabditidae; Pelodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WormPep; B0361.3; CE00752
Pfam; PF00083; sugar_tr;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 DYDEVIAFLGEWGPF------QRLIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVPD
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KNKTEKLKKY IKTANRM----
                                                                                                   R-AWITVVYNVAWSLGMVWTLLVTLMTDDWRWRYFIVSLPGVYGFALWYFLPESPHWLIT
                                                                                                                                                                                                                                                                                                                                                                                                                                -----YKNETIP-----ISETCQ------IETESSKAFGNLNGEYC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AANLSSAWRNNSVPLRLRDGREVPHSCSRYRLATIANFSALGLEPGRDVDLGQLEQESCL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPDKFVEAYGAYGKYQIFTYVLVQTLNFFYSSSMYI-----MSFVQL--NLEKQCE---
                                             QRRFREAEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQQKAFILDLFRTRNIAIMTIMSL
                                                                                                                                                      RIIFSTLGVCTFFAVGYMLLPLFAYFIRDWRMLLLALTVPGVLCVPLWWFIPESPRWLIS
                                                                                                                                                                                                              YGRKPIIVTTAILAFLANMAASFSPNFAIFLILRAFIGACSDSYLSVASVATCEYLSEKA
                                                                                                                                                                                                                                                            FGRKNVLFATMAVQTGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSV
                                                                                                                                                                                                                                                                                                                       ---GIAENTLYNVTNQKASTNLLVDFDLSCSHWFFQEFGLTIFTIGAVIAVPFMSMLADR
                                                                                                                                                                                                                                                                                                                                                                          DGWEFSQDVYL-----STVVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQLSDR
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Peloderinae; Caenorhabditis.
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20.3%;
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71 POTENTIAL.
68 POTENTIAL.
202 POTENTIAL.
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W; CBA42A80A254FB80 CRC64;
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RESULT 5
YI13_CA
ID 3_CA
ID 1-OZI
DT 01-OZI
DT 01-OZI
DT 01-OZI
DT 01-OZI
DT 02-OZI
DX 02-OZI
RN 11
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Best Local S
Matches 94
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01-OCT-1996
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Du Z., Waterston R.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 48.6 kDa protein B0252.3 in chro
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep; B0252.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                    306
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TAVPAVIEDSVEELNPLK---
                                                                                                                                                                                                                               VVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQTGFSFLQ 187
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                                                     LLAYILPDWRYLMFCISVPNIFVALLIYMTVPESLHFLVSSQQNEKIEAWLEKIRGPKGD
                                                                         LFAYFIRDWRMLLLALTVPGV-LCVPLWWFIPESPRWLISQRRFREAEDIIQK-AAKMNN
                                                                                                                         AFSTSIMMFCIMRMIHGIFYTAAGLAGWVLGYENTPLRLR-FFTSVYFGVMWVVGACFLG
                                                                                                                                                             IFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTLGVCTFFAVGYMLLP
                                                                                                                                                                                                 VADEFDLTGDASWLAESTTTFYMVGNMIGGMFIPPLADHYGRLPVFVATVLLMAVGGMIS
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435 AA;
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48571 MW;
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Caenorhabditis.
Score 307; DB 1;
Pred. No. 4.8e-13;
3; Mismatches 155
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
; 5F6160359FA1840B CRC64;
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EMBL; Z11115; CAA77460.1; -.
EMBL; Z22175; CAA77460.1; JOINED.
EMBL; Z22175; CAA80131.1; -.
EMBL; Z11115; CAA80131.1; JOINED.
PIR; S15786; S15786.
WormPep; ZK637.1; CE06638.
InterPro; IPR003562; sub_transporter.
Pfam: PF00083; Sugar_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-92168156; PubMed-1538779;
MEDLINE-92168156; PubMed-1538779;
Sulston J., Du Z., Thomas K., Wilson R., Hillier L.,
Halloran N., Green P., Thierry-Mieg J., Oiu L., Dear
Craxton M., Durbin R.K., Berks M., Metzstein M., Hawk
Ainscough R., Waterston R.;
The C. elegans genome sequencing project: a beginnin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                            PROSITE; PS00216; SUGAR_TRANSPORT_1; PROSITE; PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The C. elegans genome sequencing project: a Nature 356:37-41(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel.
01-MAR-2002 (Rel.
Hypothetical 58.3
                                                                                                                                                                          Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein (Pro-
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39, Last sequ
41, Last anno
kDa protein 2
  106
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157
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179
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                                                                                                                                               Transmembrane; Transport.

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
protein ZK637.1 in chro
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CYTOPLASMIC (POTENTIAL).
3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
4 (POTENTIAL).
                                                                                     EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL).
                                                                                                                             1 (POTENTIAL).
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S., Cou
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T.,
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RESULT 8
YCEL BA
YCEL BA
AC 034691
DT 30-MAY
DT 30-MAY
DT 30-MAY
DT 80-MAR
DE Hypoth
GN YCEL.
OS Bacill
OC Bacill
OX NCBL-1
RN (11)
RN (11)
RP SEQUEN
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034691;
30-MAY-2000
30-MAY-2000
01-MAR-2002
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                                                   Bacillus subtilis.
Bacteria; Firmicutes;
  STRAIN-168;
                              Bacillus/Staphylococcus
NCBI_TaxID=1423;
           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
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nes 110; Conserv
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(Rel.
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                                                                                metabolite
                                                                                                                                 STANDARD;
                                                                                        39, Created)
39, Last sequence up
41, Last annotation
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                                         Bacillus/Clostridium us group; Bacillus.
                                        group;
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10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
12 (POTENTIAL)
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5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
6 (POTENTIAL).
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Pred. No. 3.8
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CYTOPLASMIC (F
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8D2FF4CBA15ECD2D CRC64;
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nes 150;
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EMBL; Z99105; CAB12089.1;
Subtilist; BG12773; yceI
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PROSTITE; PS00216; SUGAR_TRANSPORT_1;
PROSTITE; PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kumano M., Tamakoshi A., Yamane K.;
"A 32 kb nucleotide sequence from the region of the lincomycin-
resistance gene (22-25 degree) of the Bacillus subtilis chromosome
identification of the site of the lin-2 mutation.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
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341 MTIMSLLLMMLTSVGYFALSLDAPN---LHGDAYLNCF----LSALIEIPAYITAWLLLR 393
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                                                          281
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                                                                                                                                                  RKNVLFATMAVQTGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEIL-----G 223
                                                                                                                                                                            GWLFDAMDVGILSFIIAALHVEWNLSPEEMKW----IGSVNSIGMAAGAFLFGLLADRIG
                                                                                                                                                                                                 GWEF-SQDV-YLSTVV----TEWNLVCED-NWKVPLTTSLFFVGVLLGSFVSGQLSDRFG 168
                                                                                                     KSVRIIFSTLGVCTFFAVGYMLLPLFAYFI---RDWRMLLLALTVPGVLCVPLWWFIPES 280
                                    PKY - - - - - - - -
                                                        PRWLISQRRFREAEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQQKAFILDLFRTRNIAI
                                                                                RVIVLLES-----FWAVGWLAAALISYFVIPSFGWQAALLLTALTAFYALYLRTSLPDS
                                                                                                                              {\tt RKKVFIITLLCFSIGSGISAFVTSLSAFLILRFVIGMGLGGELPVASTLVSEAVVPEKRG}
                                                                                                                                                                                                                        Similarity 25.
                                                                                                                                                                                                                                                                                protein;
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                                                                                                                                                                                                                                                                              ESLSAKKRSM-----
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EXTRACELLULAR (POTENTIAL).

8 (POTENTIAL).

9 (POTENTIAL).

9 (POTENTIAL).

10 (POTENTIAL).

10 (POTENTIAL).

11 (POTENTIAL).

11 (POTENTIAL).

12 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

13 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

14 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

15 (POTENTIAL).

16 (POTENTIAL).

17 (POTENTIAL).
                                                                                                                                                                                                                       Score 290; DB
Pred. No. 5.5e
68; Mismatches
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CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).

2 (POTENTIAL)
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6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
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                                    -----WARQYIR
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in no way
commercial
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yura T., Mori H., Nagai H., Nagata T., Isl
Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherichia
the 0-2.4 min region.";
                                                                                                                                                                                                                                     EMBL; D10483; BAA01321.1; ALT_FRAME. EMBL; AE000114; AAC73156.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science
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Bacteria; Proteobacteria;
                                                                     TRANSMEM
                                                                                                                  Hypothetical
                                                                                                                                      PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITION 142 AND 232 THAT PRODUCE TWO SEPARATE ORPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential).
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B., Shao Y.;
                                                                                                                                                                                                                       S40566; S40566
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                                                                                                                                                                                                     EG11566;
                                                                                                                                      PS00217;
                                                                                                      proteome
                                                                                                                                                                                     IPR003662; sub_transporter
                                                                                                                 3; sugar_tr; 1.
0216; SUGAR_TRANSPORT_1; FALSE_NEG.
0217; SUGAR_TRANSPORT_2; FALSE_NEG.
protein; Transport; Transmembrane; Inner
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Res. 20:3305-3308(1992).
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CYTOPLASMIC (POTENTIAL).

1 (POTENTIAL).

PERIPLASMIC (POTENTIAL).

2 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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Best Local Similarity
                              CSBC_BACSU STANDARD PA6333; 032289; 01-NOV-1995 (Rel. 32, C) 15-JUL-1999 (Rel. 38, L) 01-MAR-2002 (Rel. 41, L) Probable metabolite tra
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                                                                                                                                                                                                     ---MGAGISLFGLLISVAFAPETRGMSLAQT
                                                                                                                                                                                                                                  YIVMGSLTVLIG - - IFTLFFPESLGMTLPET 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLCVPLWWFIPESPRWLISQRRFREAEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQQKA
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                                                                                                                                                                                                                                                                       FFSGGPGNLQWLYPNELFPTDIRASAVGVIMSLSRIGTIVSTWALPININNYGISNTML-
                                                                                                                                                                                                                                                                                                      AES-----MLYVETAELYPTLVRNMAVGVTSTASRVGSIIA----PYEV-YLGAYNRMLP
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                                  transport
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25.8%;
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Last annotation update
                                                                                    Created)
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CYTOPLASMIC (POTENTIAL)
5 (POTENTIAL)
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FSSIH -> CLLHY (IN REF. 1).

D -> Y (IN REF. 1).

L -> F (IN REF. 1).

T -> N (IN REF. 1).

R -> C (IN REF. 1).

N -> S (IN REF. 1).

N -> D (IN REF. 1).
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Pred. No. 6.2e
76; Mismatches
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9 (POTENTIAL).
PERIPLASMIC (P
10 (POTENTIAL).
CYTOPLASMIC (P
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8 (POTENTIAL)
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CYTOPLASMIC (17 (POTENTIAL)
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F => L (IN REF. 1).
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12 (POTENTIAL).
                                  protein
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                                  n update)
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5.2e-11:
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use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a lloense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Microbiology 145:1069-1078(1999).
-I- FUNCTION: COULD SERVE EITHER A NUTRITIONAL OR AN OSMOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168 / BGSC1A1;
MEDLINE=96093926; PubMed=7584049;
Yoshida K.-I., Seki S., Fujimura
                       DOMAIN
TRANSMEM
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 299124; CAB16017.1; -.
Subtilist; BG11360; csbC.
InterPro; IPR003663; Sugar_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restitute the company of the comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION. MEDLINE=99303315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujita Y., Shibayama T., Submitted (JUN-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                     Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00216; SUGAR_TRANSPORT_1; PROSITE; PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00083; sugar_tr; 1. PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunst F., Ogasawara N., Submitted (NOV-1997) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003662; sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
     PubMed=10376822;
     Yoshikawa H., Danchin the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishio I., Aoyama D., Yoshida K. the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
CYTOPLASMIC (POTENTIAL).
1 (POTENTIAL)
10 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

11 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)
                                                                                                                              EXTRACELLULAR (POTENTIAL)
8 (POTENTIAL)
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4 (POTENTIAL)
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2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
3 (POTENTIAL).
                                                                                            CYTOPLASMIC
9 (POTENTIAL
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7 (POTENTIA)
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6 (POTENTIAL)
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databases
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the Bacillus subtilis
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Best Local Sim
Matches 118;
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CONFLICT
SEQUENCE
                                                                                                                        Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                       Hypothetical n
YGCS OR B2771.
                                                                                                                                                                                                                                                             Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                    01-MAR-2002
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                                                                                                Science
                                                                                                                                                                            MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                  NCBI_TaxID=562;
                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                                                                                                                                                                                01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                             Q46909;
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                                                      -!- SIMILARITY:
                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                 SUBCELLULAR LOCATION:
                                                                      (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           KSL-EETEASLK-KRFKKKKSTQNQVLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTLPETLEQMQKVKWFRSGKKTRDSMETE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRIIFSTL-----GVCTFFAVGYM 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTAVPAVIFDSVEELNPLKQ----QKAFILDLFRTRNIAIMTIMSL-LLWMLTSVGYFAL 359
                                                                                                                                                                                                                                                                                                                                                                         ECOLI
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461 AA;
                                                                                                                                                                                                                                                                        coli.
                                                                                                                                                                                                                                                                                                   (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
metabolite transport protein ygc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403
                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                       BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -WRWMVGLAAVPAVLLLIGIAFMPESPRWLVKRGSEEEARRI-----MN
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Pred. No. 1
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CYTOPLASMIC (POTENTIAL).
RP -> SA (IN REF. 3).
B6587B5DC7272EF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                       SUGAR TRANSPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                             subdivision;
                                                                                membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541
                                                                                                                                                                                                                                                                                                                                                                        445 AA.
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                                                                                 membrane
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Matches
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Best Local
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TRANSMEM
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DOMAIN
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EcoGene; EG13126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tities requires a license agreement (seement an email to license@isb-sib.ch).
                                                                 YVVAFILGTBILGKSVR-IIFSTLGVCTFFAVGYMLLPLFA-YFIRD----WRMLLLALT
                                                                                                                                                                                                                    VPGVLCVPLWWFIPESPRWLISQRRFREAEDIIQKAAKMNNTAVPAVIFDSVEELNPLKQ
 VLAQWGMQVTLLLLATVLLVGFVVTWLWAPETKALPL
                                                 VLFSTTISAVSNLVGILPAESFPTDIRSLGVGFATAMSRLGAAVS---
                                                                                                   ALTASLMLNALLIVGALLGLVLTHLLAHRKFLLGSFLLLAATLVVMACLPSGSSLTLLLF
                                                                                                                          FLSALIEIPAYITAWLLLRTLPRRYIIAAVLFWGGGVLLFIQLVPV----DYYFLSIGLV
                                                                                                                                                                            QKAFILDLFRTRNIAIMTIMSLLLWMLTS-----VGYFALSLDAPNLHGDAYLNC
                                                                                                                                                                                                     LPALLITLLRWGTPESPRWLLRQGRFAEAHAIVHRYFG-----PHVLLGD------
                                                                                                                                                                                                                                                    YSVGHTLLAEFSPRRHRGILLGAFSV--VWTVGYVLASIAGHHFISENPEAWRWLLASAA
                                                                                                                                                                                                                                                                                                      LGLFLGSLVLGWISDHIGRQKIFTFSFLLITLASFLQFFATTPEHLIGLRILIGIGLGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U29579; AAA69281.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                       96;
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PS00217; SUGAR_TRANSPORT_2;
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                                                                                                                                                  -EVVTATHKHIKTLFSSRYWRRTAFNSVFFVCLVIPWFVIYTWLPTIAQTIGLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                             11 (POTENTIA
PERIPLASMIC
12 (POTENTIA
                                                                                                                                                                                                                                                                                                                                                                 Score 262; DB 1
Pred. No. 4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                              12 (POTENTIAL)
CYTOPLASMIC (F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 (POTENTIAL)
CYTOPLASMIC (
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PERIPLASMIC (
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CYTOPLASMIC (
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10 (POTENTI
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                                                                                                                                                                                                                                                                                                                                                                                                                  TOPLASMIC (POTENTIAL). B59E452721B15774 CRC64;
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  429
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                                                                                                                                                                                                                                                                                                                                                       162;
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                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                           490
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                                                                                                                          430
                                                                                                                                                                                                                            324
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                                                                                                                                                                                                                                                                             264
                                                                                                                                                                                                     227
                                                                                                                                                                                                                                                                                                                                                       11;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Solute carrier family 2, facilitated (
                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96157892; PubMed=8589457;
Wagsttaff P., Kang H.Y., Mylott D., Robbins P.J., White M.K.;
"Characterization of the avian GLUT1 glucose transporter:
differential regulation of GLUT1 and GLUT3 in chicken embryo
                                                                                                                                                                                                                                                                                                                         EMBL; L07300; AAB02037.1;
InterPro; IPR003563; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRENNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHICK
            TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                             Transmembrane;
Multigene fami
                                                                                                                                                                                                                                                                                      PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transmembrane; Sugar transport; Transport; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Glucose transporter type 1) (GT1). SLC2Al OR GLUT1.
                                                 TRANSMEM
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                                                                           TRANSMEM
                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM MAY BE RESPONSIBLE FOR CONSTITUTIVE OR BASAL GLUCOSE UPTAKE. HAS A VERY BROAD SUBSTRATE SPECIFICITY. CAN TRANSPORT A WIDE RANGE OF ALDOSES INCLUDING BOTH PENTOSES AND HEXOSES (BY SIMILARITY).

SUBCELLULAR LOCATION: Integral membrane protein. Localizes primarily at the cell surface (By similarity).

SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSPORTER SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHICK
                                                                                                                                                                                                                                                                             family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 6:1575-1589(1995).
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neognathae;
Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                8 (POTENTIAL).
CYTOPLASMIC (F
                                                                                                    CYTOPLASMIC
7 (POTENTY)
                                                                                                                                      5 (POTENTIAL)
EXTRACELLULAR
                                                                                                                                                    CYTOPLASMIC
5 (POTENTIA:
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1 (POTENTIAL
             CYTOPLASMIC
                                     EXTRACELLULAR
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                        10 (POTENTIAL)
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on update)
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Best Local Sir
Matches 117;
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SEQUENCE
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DOMAIN
SITE
                                                                                                                                                                                                                                              YEAST
                                                                                                                                                                                   P38695;
P1-FEB-1995 (Rel. 31, Created)
O1-FEB-1995 (Rel. 31, Last sequence update)
O1-MAR-2002 (Rel. 41, Last annotation updat
                                                                  STRAIN-MC996;
Reifenberger E.,
                                                                                                                           Eukaryota; Fungi; A
Saccharomycetales;
                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                              HXT5 OR YHR096C.
                                                                                                                                                                          Probable glucose transporter HXT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
Johnston M., Andrews S., Brinkman
                                                                                            SEQUENCE
                                                                                                                NCBI_TaxID=4932;
                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156
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                                   SEQUENCE FROM
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17; Conservative
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449
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54086
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                                                          EMBL/GenBank/DDBJ
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Pred. No. 3.5e-09;
7; Mismatches 170;
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DEFINES SUBSTRATE SPECI
SIMILARITY).
N-LINKED (GLCNAC. . . )
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12 (POTENTIAL).
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Ωy 밁

124 YLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQTGF 183

RTGLMVSIFNIGCAIGGIVLSKLGDMYGRKIGLMTVVVIYSIG

177

130

YLSDV--

Query Match Best Local Similarity

8.7%;

Score Pred.

247; DB 1 No. 5e-09;

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Length 592;

Indels

142;

Gaps

22;

Matches

Conservative

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InterPro; IPR003662; sub_transporter.
Pfam; PP00083; sugar_tr; 1.
PRINTS; PR00171; SUGAT_TRANSPORT_1; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_2; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Du Z., Favello A., Fulton L., Gattung S., Gei
Kucaba T., Hillier L., Jier M., Jöhnston L.,
Latreille P., Louis E.J., Macri C., Mardis B.
Nhan M., Rifkin L., Riles L., St Peter H., Tr
Vignati D., Wilcox L., Wohldman P., Waterstor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of Saccharomyces cerevisiae \ensuremath{\text{VIII.}}\ensuremath{\text{"}};
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                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: PROBABLE GLUCOSE TRANSPORTER.
SUBCELLAULAR LOCATION: Integral membrane protein.
MISCELLAUROUS: GLUCOSE TRANSPORT IS THOUGHT TO B
KINETICALLY DISTINCT SYSTEMS, A GLUCOSE-REPRESSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM AND A CONSTITUTIVE LOW-AFFINITY SYSTEM. SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                             Transmembrane; 81
  385
403
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  AA;
            Sugar
   M.
                                                                                                        8 (POTENTIAL).
CYTOPLASMIC (POTENTT:
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transport; Transport; Glycoprotein.
  N-LINKED (GLCNAC. ..) (P
N-LINKED (GLCNAC. ..) (P
, 6906721BAC1A5F87 CRC64;
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Trevaskis E., Vaughan F
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15-JUL-1999 (Rel. 38, Cre
15-JUL-1999 (Rel. 38, Las
01-MAR-2002 (Rel. 41, Las
Hypothetical metabolite t
                    MEDLINE-97251357; PubMed-9097039;
Alba H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
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Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
"A 570-kb DNA Sequence of the Escherichia coli K-12 Genome
Corresponding to the 28.0-40.1 min Region on the Linkage Map.";
DNA Res. 3:363-377(1996).

DNA Res. 3:363-377(1996).
                                                                                                                                                                                                 STRAIN-KI
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           Science
                                                                                                                                                                                                                                                                      Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
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MEDLINE-97426617; Pu
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Bacteria; Proteobacteria;
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PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
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                RYIIAAVLFWGGGVLLFIQLVPVDYYFLS--IGLVMLGKFGITSAFSMLY-----VFTA 449
                                     CVLIAMNVVQYTLINWLPTIFMTQGINLKDSIVLNTM--SMFGAPFGIFIAMLVMDKIPR
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97; Conser
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01-OCT-1996 (Rel. 34,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long
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NCBI_TaxID=28985;
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Eukaryota; Fungi; Ascomycota;
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PROSITE; PS00217; SUGAR_TRANSPORT_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
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SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: PROBABLE GLUCOSE TRANSPORTER.
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cetaceae; Kluyveromyces
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CYTOPLASMIC (POTENTIAL).
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                                                            WAPIAYVVVAESYPLRVKAKCMAIATASNWIWGFLNGFFTPFITSAIHFYYGYVFMGCLV
                                                                                                                         LWGAAAMTACMVV----FASVGVTRLWPDGANHPETASKGAGNCMIVFACFYIFCFATS
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                                                                                        AFSMLYVFTAELYPTLVRNMAVGVTSTASRVGSIIAPYFV--YLGAYNRMLPYIVMGSLT 497
                                                                                                                                                                                         NYFFYYGTTIFNSVGMD-----DSFETSIVLGIVNFASTFVAIYVVDKFGRR----KCL
                               VLIGIFTLFFPESLGMTLPETLEQMQK-----VKWFRSGKKTR----DSMETEENP 544
AMFFYVFFFVPETKGLTLEEVQEMWEEGVLPWKSSSWVPSSRRNAGYDVDALQHDEKP 560
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06; Conservative
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Pred. No. 6.4e-09;
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Search completed: July 17, Job time: 662 sec 2002, 02:15:01

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
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     SPTREMBL_19:*

1: sp_archea:*
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3: sp_fungi:*
4: sp_numan:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_vortebrate
13: sp_vertebrate
14: sp_unclassifi
15: sp_archeap:*
16: sp_bacteriap:
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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2845
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sp_organelle:*
sp_phage:*
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sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	œ	7	6	5	4	ω	2	1	Result No.
709	754.5	754.5	773.5	781.5	794.5	815	819	852	857	2034.5	2211	2470	2484	2833	2845	Score
24.9	26.5	26.5	27.2	27.5	27.9	28.6	28.8	29.9	30.1	71.5	77.7	86.8	87.3	99.6	100.0	Query Match Length
540	576	568	561	563	577	567	567	548	548	564	557	553	553	551	551	Length I
11	ഗ	u	U	ഗ	4	σ	ഗ	ഗ	5	11	4	11	11	4	4	BB
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Q91wu2 mus musculu	002270 caenorhabdi	Q9u539 caenorhabdi		Q95tw6 drosophila		Q95r48 drosophila	Q9vca3 drosophila	001384 drosophila	Q9vca2 drosophila	Q9wtn6 mus musculu	Q96eh6 homo sapien	Q9z306 mus musculu	Q9r141 rattus norv	Q9h015 homo sapien	O14546 homo sapien	Description

44 648											_				27 688.5								~1	7	7
40 22.8	22	22.	22.	23.	23.	23.	23.	23.	23.	ω.	24.	24.	24.	24.	24.	24.	24.	24.	24.	24.		24.	0 24.	03 24.7	7 2
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ALIGNMENTS

Qy Db	Qu Be Ma	SQ	DR DR	DR	33	C R	RT	RT	RX	RC	RP	RN	S S	88	So	GN	DE	DT.	Di	AC	Ħ	RESULT
1 MRDYDEVIAFLGEWGPFORLIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVPDAANLSS 60 	Query Match 100.0%; Score 2845; DB 4; Length 551; Best Local Similarity 100.0%; Pred. No. 7.5e-200; Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 551 AA; 62177 MW; F5903421C789F60A CRC64;	PIAM; PFUUU83; SUGAR_TRANSPORT_1; UNKNOWN_1. TROSTER PRO0216; SUGAR_TRANSPORT_1; UNKNOWN_1.	Interpro: IPR003662; sub_transporter.	-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.	FEBS Lett. 419:107-111(1997)I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	cation transporter, OCTN1.";	"Cloning and characterization of a novel human pH-dependent organic	MEDLINE=98086199; PubMed=9426230;	TISSUE=LIVER;	SEQUENCE FROM N.A.			Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.).	OCTN1.	OCTN1.	01-DEC-2001 (TremBLrel. 19, Last annotation update)	(TrEMBLrel. 05,		O14546 PRELIMINARY; PRT; 551 AA.	77 1

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Matches 549
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Q9H015;
Q9H015;
Q9H015;
Q1-MAR-2001 (TrEMBLrel. 16, Cr
Q1-MAR-2001 (TrEMBLrel. 19, Le
Q1-DEC-2001 (TrEMBLrel. 19, Le
Q1-DEC-2001 (TREMBLREL TRANSPORT P)
                                                                                                                                           SEQUENCE FROM N.A.

Spritzenberger F., Gruendemann D., Scho
Spritzenberger F., Gruendemann D., Scho
Submitted (DEC-1996) to the EMBL/GenBan
-!- SUBCELLULAR LOCATION: INTEGRAL MEMB
-!- SIMILARITY: BELONGS TO THE SUGAR TR
EMBL; Y09881; CAA71007.1; -.
InterPro; IPR003662; sub_transporter.
Pfan; PF00083; sugar_tr; 1.
                                                                                                                           Transmembrane.
SEQUENCE 551
                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                          emann D., Schoemig E.;
he EMBL/GenBank/DDJ databases.
INTEGRAL MEMBRANE PROTEIN (BY
O THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                         , Created)
, Last sequence upo
, Last annotation of PROTEIN.
                                                                     Score 2833; DB 4;
Pred. No. 5.7e-199;
0; Mismatches 2;
                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Q9R141;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
ORGANIC CATION TRANSPORTE
                                            Transmembrane.
SEQUENCE 553
                                                         - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROPERTY: BELONGS TO THE SUGAR TRANSPORTED EMBL; AF169831; AAD46922.1; - InterPro; IPR003662; sub_transporter. Pfam; PF00083; sugar_tr; 1. PF005TTE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
                                                                                                                                                                                                       OCTN1.

Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=20286310; Pu
Wu X., George R.L.,
                                                                                                                  placenta.";
Biochim. Biophys.
                                                                                                                                                      Ganapathy
                                                                                                                                  pattern of OCTN1,
                                                                                                                                             "Structural
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           Similarity
                                                                                                                                 and functional characteristics OCTN1, an organic cation transpo
 Conservative
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                                                                                                                                                                                                                                            TRANSPORTER
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                                                                                                                                                            PubMed=10825452;
                                                                                                                  Acta
                                                                                                                                                                                                         Chordata;
Rodentia;
                                            62362 MW;
          87.3%;
85.2%;
                                                                                                                  1466:315-327(2000)
                                                                                                                                                                                                                                                    13,
 36;
                                                                                                                                                                                                                                           , Last sequence update) , Last annotation updat OCTN1.
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Score 2484; DB 11;
Pred. No. 1.7e-173;
6; Mismatches 44;
                                                                                                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                       PRT;
                                            E26C8155768A14AD CRC64;
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AR TRANSPORTER
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transporter,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                    Tamai I., Ohashi R., Nezu J., Sai Y., Koba)
Shimane M., Tsuji A.;
"Molecular and Functional Characterization
Transporter Family in Mice.";
J. Biol. Chem. 275:40064-40072(2000).
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C57BL 6J; TISSUE-KIDNEY;
MEDLINE-20568258; PubMed=11010964;
Submitted (JUL-2001) to the EMBL/GenBank/DDbJ databases.
i- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY
i- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
EMBL; AB016257; BAA36626.1; -.
EMBL; BC010590; AAH10590.1; -.
MGDJ: MGI1353479; S1022a4.
InterPro; IPR003662; sub_transporter.
                                                                                                                              Strausberg R.;
Submitted (JUL
                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-BREAST TUMOR;
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Q95EH6, PTELLMINARY; PKI; J, ....
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO SOLUTE CARRIER FAMILY 22 (ORGANIC CATION
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PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
Transmembrane.
SEQUENCE 553 AA; 62290 MW; C4D66BC061398653
SEQUENCE FROM N.A.
TISSUB-LUNG CARCINOMA;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC012325; AAH12325.1; -.
SEQUENCE 557 AA; 62735 MW; 9C3E15059F20E6A4 CRC64;
                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                            NCBI_TaxID=9606;
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                                            MEDLINE=20568258; PubMed=11010964;
Tamai I., Ohashi R., Nezu J., Sai Y., Kobayas Shimane M., Tsuji A.;
Shimane M., Tsuji A.;
"Molecular and Functional Characterization of Transporter Family in Mice.";
J. Biol. Chem. 275;40064-40072(2000).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE I--1- SIMILARITY: BELONGS TO THE SUGAR TRANSPOREMEL, ABO18436; BAA7843-1;
MGD; MGI:1929481; Slc22a9.
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Q9WTN6;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE-TESTIS;
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interPro; IPR003662; sub_transporter
fam; PF00083; sugar_tr; 1.
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Pred. No. 1
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ORCT PROTEIN (GH216559).
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Transmembrane.
SEQUENCE 564
                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyo;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer
                                                                                                                  SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRDYDEVIAFLGEWGPFQRLIFFLLSASIIPNGFNGMSVVFLAGTPÄHRCRVPDAANLSS
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Conzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY EMBL; AE003747; AAF56271.1; -. EMBL; AY058437; AAL13666.1; -. FlyBase; FBgn0019952; Orct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin
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                                                                                                                                                                                                                                                                                                                                      EQESCLDGWEFSQDYYLSTVYTEWNLVCEDNWKVPLTTSLFFVGYLLGSFVSGQLSDRFG
                                                                                                                                                                                                                              PHLWNLSYPENER --
RKPTFFASLVLQLIFGVLAAVAPEYFSYTISRMIVGATTSGVFLVAYVIALEMVGSSYR-
                                                                                                                                                                                                                                                                                     SAWRNNSVPLRLRDGREVPHSCSRYRLATIANFSALGLEPGRDVDL----
                                                RKNVLFATMAVQTGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003662; sub_transporter
                                                                                                          -SSYVYDRSKYLNSAVTEWNLVCSRSLLSATSDSLFMLGVLLGSLIFGQMSDKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.1%;
                                                                                                                                                                                                                              ----CSYY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 857; DB 5;
pred. No. 1.1e-54;
98; Mismatches 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08D7F97599B477AF CRC64;
                                                                                                                                                                                                                           ------DVDYTEEYLNGSIPRSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                     -GQL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-98072431; PubMed-9409773;

Taylor C.A.M., Stanley K., Shirras A.D.;

Taylor Cret gene of Drosophila melanogaster codes cation transporter with six or 12 transmembrane Gene 201:69-74(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 01-OCT-2001 (TrEMBLrel. PUTATIVE ORGANIC CATION
                                                                                                                                                                                                                                                                                              EMBL; X12400; CAA73031.1; -.
FlyBase; FBgn031652; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
                                                                                                                                                                                                                                                                   Transmembrane.
SEQUENCE 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORCT OR CG6331.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFSTLGVCTFFAVGYMLLPLFAYFIRDWRMLLLALTVPGVLCVPLWWFIPESPRWLISQR
RKNVLFATMAVQTGFSFLQIFSISWEMFTVLFVIVGMGQISNYVVAFILGTEILGKSVRI 228
                          ETKTC-SSYVYDRSKYLNSAVTEWNLVCSRSLLSATSDSLFMLGVLLGSLIFGQMSDKLG
                                            EQESCLDGWEFSQDYYLSTVVTEWNLVCEDNWKVPLTTSLFFVGVLLGSFVSGQLSDRFG 168
                                                                                                            EDGENF - - - - - GKKPAPQETAEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMTIMSLLLWMLTSVGYFALSLDAPNLHGDAYLNCFLSALIEIPAYITAWLLLRTLPRRY
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                                                                                                                                          YDDVITHLGEFGPYQKRIYYLLCLPAIVCAFHKLAGVFLLAKPDFRCALPYENGSIYELS
                                                                                                                                                                                                Similarity 35.!
00; Conservative
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35.5%;
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04, Last sequence update)
18, Last annotation updat
TRANSPORTER.
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                                                                                                                                                                                                core 852; DB 5;
red. No. 2.7e-54;
Mismatches 208
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                                                                                   -DVDYTEEYLNGSIPRSSN
                                                                                                                                                                                                                         Length 548;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Rachards S., Ashburner M., Henderson S.N.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Doublos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Harris N.J., Evangelista C.C., Ferraez C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Hostin O., Nelson D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9VCA3;
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-JUN-2001 (TrEMBLrel. 1
CG13610 PROTEIN.
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13,
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                                                       Q95R48
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EMBL; AE003747;
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InterPro; IPR003662; sub_transporter
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Q96RU0;
O1-DEC-2001 (TrEMBLrel. 19, 0)
O1-DEC-2001 (TrEMBLrel. 19, 0)
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ORGANIC CATION TRANSPORTER O
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular identification OKB1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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Mammalia; Eutheria;
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532
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                                                                      LVRNMAVGVTSTASRVGSIIAPYFVYLGAYNRMLPYIVMGSLTVLIGIFTLFFPESLGMT
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LATTWEEAAKL
                                                                                                VGRRTYLAYSLFCSALACGVVMVIPQKHYILGVVTAMVGKFAIGAAFGLIYLYTAELYPT
                                                                                                                                                                                                PFWLLSEGRYEEAQKIVDIMAKWNRASSCKLSELLSLDLQGPVSNSPTEVQKHNLSYLFY
                                                IVRSLAVGSGSMVCRLASILAPFSVDLSSIWIFIPQLFVGTMALLSGVLTLKLPETLGKR
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  ESENESKSSKLLLT
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Pred. No. 4.4e-50;
17; Mismatches 222;
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095TW6;
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01-DEC-2001
01-DEC-2001
01-DEC-2001
GH27944P.
CG4630.
                                   Drosophila
Eukaryota;
         Pterygota; Neopt
Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                        Q95TW6
                                                                                                                        12
                 melanogaster (Fruit fly).
metazoa; Arthropoda; Tracheata; Hexapoda;
Neoptera; Endopterygota; Diptera; Brachyce
a; Drosophilidae; Drosophila.
                                                                     (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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Last sequence up
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                           Brachycera;
                                    Insecta;
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Q9V6L6;
Q9V6L6;
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01-MAY-2000
01-JUN-2001
CG4630 PROTE
CG4630.
                                                                             Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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STRAIN-Y, CN BW SP;

STRAIN-Y, CALSON

J. Pares S. Phouanenavong S.,

YU C., Lewis S.E., Rubin G.M., Celniker S.;

SUbmitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY08475; AAL13704.1; -

SEQUENCE 563 AA; 62138 MW; D3E2CB4096A195CB CRC64;
     SEQUENCE
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SYYDPLPLLLFGTLSLVAGLLSLLLPETFNRKLPDTVEE
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Pred. No. 3.8e-49;
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ingall C.
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Ra Ra Man K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G., Ra Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baidwin D., Balley R.M., Basa Q., Barshala J., Bayrakkaroglu L., Beasley E.M., Ra Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burtler R., Sarchala J., Bayrakkaroglu L., Beasley E.M., Ra Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Broktler P., Borthan M.R., Bouck J., Brokstein P., 
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0033809; CG4630.
InterPro; IPR003662; sub_transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE EMBL; AE003819; AAF58407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
                                               214
                                                                                      184
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                                                                                                                                                                                                                                                                                                                                                         DYDEVIAFLGEMGPFQRLIFFLLSASIIPNGFNGMSVVFLAGTPEHRCRVPDAANLSSA-
AFIGVEMVGPRKREM-SSIVLNYFYAVGEALLGL-SVFLPDWRQLQLALSVPPLICVAY
                                         AFILGTEILGKSVRIIFSTLGVCTFFAVGYMLLPLFAYFIRDWRMLLLALTVPGVLCVPL
                                                                                                                                                                                       LEQESCLDGWEFSQDVYLS---TVVTEWNLVCEDN-WKVPLTTSLFFVGVLLGSFVSGQL 163
                                                                                      ADRYGRKHI
                                                                                                                        SDRFGRKNVLFATMAVQTGFSFLQIF-----SISWEMFTVLF--VIVGMGQISNYVV
                                                                                                                                                                                                                                                 YGANWVSTAVPGSWSKRGHFTPSTCERF----VANGDHLESSSDPWSAWPLDQCFAENFT 129
                                                                                                                                                                                                                                                                                          ----WRNNSVP-LRLRDGREVPHSCSRYRLATIANFSAL--GLEPGRDVDLGQ-----
                                                                                                                                                                                                                                                                                                                                   DEDDILVEIGEFGREQRRNYLLICLPVLFAAANSLSYVFTAGSPTYRCYVPECDKLVDAE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00083; sugar_tr;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                  -NQFVYGSSERTIVQQWGLQCPENLWKLAFVGTIHFAGLVVGTALSGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62041 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                    27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                     118;
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THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 773.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       573643481595788F CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                 .5e-48;
nes 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                   95;
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                                                                                                                                                                                   Query Match
Best Local
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TIEMBLICAL. 13, Created)
01-MAY-2000 (TIEMBLICAL. 13, Last sequence update)
01-DEC-2001 (TIEMBLICAL. 19, Last annotation update)
ORGANIC CATION TRANSPORTER 1 (F52F12.1B PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=99227113; PubMed=10209228;
Wu X., Fei Y.J., Huang W., Chancy C., L

"Identity of the F52F12.1 gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCT-1 OR F52F12.1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9U539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organic cation transporter
                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: BELONGS TO THE SUGAR EMBL; AF110415; AAF21932.1; -. EMBL; Z83228; CAC70093.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matthews
                                                                                                                                                                                                                                                                          Transmembrane.
SEQUENCE 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C.elegans: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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WRNNSVPLRLRDGREVPHSCSRYRLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFSQ
                                                                 PF00083; sugar_tr;
                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                   IPR003662; sub_transporter.
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                                                                                                                                                           Conservative
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cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                               63505 MW;
                                                                                                                                                                                   26.5%;
30.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            INTEGRAL MEMBRANE
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                                                                                                                                                             Score 754.5; DB 5;
Pred. No. 3.6e-47;
9; Mismatches 236;
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                                                                                                                                                                                                                                                                               COA3E73851F44056 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leibach F.H.,
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in Caenorhabditis elega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tion update) PROTEIN).
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DYDEVIAFLGEWGPFQRLIFFLLS-ASIIPNGFNGMSVVFLAGTPEHRCRVPDAANLSSA

Query Match Best Local S Matches 169

Similarity

26.5%;

Conservative

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Science 282:2012-2018(1998).
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Pfam; PF00083; sugar_tr; 1.
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/dev_stage="fetal"
/note="inbetween D58642
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KEYWORDS
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integral membrane phuman.
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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Spritzenberger, F., Gr
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Submitted (05-DEC-1996) D. (
Department Of Pharmacology,
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                                                             note="putative"
                                                                     /gene="UT2h"
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61.4%; 85.7%;

Score 1310.6; Pred. No. 2.4e-0; Mismatches

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BASE COUNT	gene CDS	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	ACCESTION VERSION VERSION VERSION VERSION VERSION CERTON SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL PUBMED	
/coden_start=1 /coden_start=1 /product="OCTN1" /product="	musculu 6J" 10090" kidney" ult"	2 (bases 1 to 2083) Nezu,J. Direct Submission Submitted (15-JUL-1998) Jun-ichi for Molecular Medicine, Inc., Ge Nihari, Ibaraki 300-4101, Japan Tel:81-298-30-6211, Fax:81-298-3 Location/Qualifiers 1. 2083	Mus musculus mRNA for OCTN1, complete cds. ABO16257.1 GI:4126604 OCTN1; organic cation transporter. Mus musculus (strain:C57BL 6J) adult kidney cDNA to mRNA. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (sites) 1 (sites) Tamai, I. Ohashi, R., Nezu, Ji., Sai, Y., Kobayashi, D., Oku, A., Shimane, M. and Tsuji, A. Molecular and Functional Characterization of Organic Catton/Carnitine Transporter Family in Mice J. Biol. Chem. 275 (51), 40064-40072 (2000)	agtotcottactcatt

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BC010590
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          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Baylor College of Medicine Human Sequencing Center Center code: BCM-HGSC
                                                                                                                                      Direct Submission
Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                         NIH-MGC Project URL: http://m
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar He
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Mammalia; Eutheria;
1 (bases 1 to 2277)
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http://www.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4126604. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
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/protein_id="AAH10590.1"
/protein_id="AAH10590.1"
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/db_xref="g::14
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/tissue_type="Mammary tumor. WAP-TGF alpha model.
old, gross tissue."
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/db_xref="LocusID:30805"
/db_xref="taxon:10000"
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/lab_host="DH10B"
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8 GATGCTGCTGGCCTGACACTGCCTGGCCTGTTCTGTGTTTCCCCTGTGGTGGTTTTTA	Db	
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Structural and functional characteristics and tissue pattern of rat OCTN1, an organic cation transporter, placenta
Biochim. Biophys Act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu.X., Wang,H., Leibach,F.H. and June L. Leibach,F.H. and June Lirect Submission
Direct Submission
Submitted (17-JUL-1999) Department of Biochemistry and Molecular Submitted (17-JUL-1999) Department of Biochemistry and Molecular Biology, Medical College of Georgia, 1120 15th Street, Augusta, (
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/protein_id="AAD46922.1"
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/translation="MRDYDEVIAFLGDWGPFQRLIFFLLSASIIPNGFNGMSVVFLAG
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VDLEQLEGECLDGWEYSKDVFLSTIVTEWNLYCEDWFPLTTSIFFVGVLCGFVVS
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TPESSPNGLISGRRFEERBEDIIQKAARKNGIMAPAVITDPLEIGELNSLKQGKVEILDL
                                                                                                                        FKTRNIATITVMSVMLWMLTSVGYFALSLNVPNLHGDVYLNCFLSGLIEVPAYFTAWL
LLATIJPRRYIIAGVILFWGGGVILLLVQVVPEDYNFVSIGLVVLGKFGVTSARSMLXVFT
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FPESFGVTLJENLEQMQKVRGFRCGKKSTVSMDREENPKVLITAF*
565 c 566 g 569 t
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/db_xref="taxon:10116"
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                                                                                                                                     Direct Submission
Submitted (28-MAY-1998) Jun-ichi Nezu, Chugai Research Institute for Molecular Medicine, Inc., Gene Search Program; 153-2 Nagai, Niihari, Ibaraki 300-4101, Japan (E-mail:nezuj@cimmed.com, Tel:81-298-30-6211, Fax:81-298-30-6270)
                                                                                                                                                                                                                                                                                                                1831
Homo sapiens mRNA for OCTN2,
AB015050
                                                   Sal,Y. and Tsujl,A. Molecular and functional identification of sodium high affinity human carnitine transporter OCTN2 J. Biol. Chem. 273 (32), 20378-20382 (1998) 98352077
                                                                                                                    Tama:
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1. .1831
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                                                                                                                 Ohashi, R., Nezu, J.,
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124. . 1797
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acagtgtcccgctgcggctgcgggacggccgcgaggtgccccacagctgcagccgctacc 399
                                                                                                                                                                                                                                                                                                       acgaggtgatcgccttcctgggcgagtgggggcccttccagcgccctatcttcttcctgc 219
                                                                                                                     ccccggagcaccgctgtcgagtgccggacgccgcgaacctgagcagcgcctggcgcaaca 339
                                                                                                                                                                                           TCAGCGCCAGCATCCCCAATGGCTTCACCGGCCTGTCCTCCGTGTTCCTGATAGCGA
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                                                                                                                                                                                                                                                                                      ACGAGGTGACCGCCTTCCTGGGCGAGTGGGGGCCCTTCCAGCGCCTCATCTTCCTGC
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AF057164.1
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Wu,X., Prasad,P.D., Leibach,F.H. and Ganapathy,V.
cDNA sequence, transport function, and genomic organization
human OCTN2, a new member of the organic cation transporter
Biochem. Biophys. Res. Commun. 246 (3), 589-595 (1998)
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College of Georgia, 1120
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resprotpldptioplrywgmkirkxtpshtrmlkdggerptilkstaf"
lessrotpldptioplrywgmkirkxtpshtrmlkdggerptilkstaf"
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; Pred. No. 2.2e
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0 15th Street, Augusta, GA 30912-2100,
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1293 1374	ctcctaatttacatggagatgcctacctgaactgtttcctcttctgccttgattga	1234 1315	D 24
		25	Dp.
1254 1233	CAACAGTCCCACAACATTCTGGATCTGCTTCGAACCTGGAATATCCGGATGGTCACC	1195 1174	OV DB
1173	gcagcagaaagctttcattctggacctgttcaggactcggaatattgccataatgacca	1114	Qy
1113 1194	acacagctgtaccagcagtgatatttgattctgtggaggagctaaatcccctga	1060	D 04
1134	CAGGGACGATTTGAAGAGGCAGAGGCTGATCATCCGCAAAGGCTGCCAAAGCCAATG	1075	Дb
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1014	TGCTGCCACTGTTTGCTTACTTCATCCGAGACTGGCGGATGCTGCTGGTGGCGCTGACGA	955	В
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⊣	GGTGTGCTGTTGGGCTCCTTCATTTCAGGGCAGCTGTCAG	Ü	dd .
639	cacctccctgttcttcgtaggcgtgctcctcggctccttcgtgtccgggcagctgtcag	æ	Qy
654	Cyticoaccyticgtigatecyapatictygtgtgtgtgaggacactggaaggtgcccctca	595	B &
y y	GGGCCAGCTGGAGCAGGAGCTGTCTGGATGGCTGGGAGTTCAGTCAG) W) B
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534	GGCTCGCCACCATCGCCAACTTCTCGGCGCTCGGGCTGGAGCCGGGGCGCGACGTGGACC	475	рb
459	getegecaceategecaactteteggegetegggeteggageegggggegaegtggace	400	Qy

FEATURES source	REMARK COMMENT	AUTHORS TITLE JOURNAL	KEYMORDS SOURCE ORGANISM REFERENCE	RESULT 8 BC012325 LOCUS DEFINITION ACCESSION	Qy 1774 atc 	Qy 1714 ag Db 1795 Ta	Qy 1654 tc. Db 1735 TC	Qy 1594 ct Db 1675 CC	Qy 1534 tc 	Db 1555 TG
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 29 Row: a Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 3273740. Location/Qualifiers 1. 2811 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MGC:20139 IMAGE:4548603" /tissue_type="Lung, large cell carcinoma"	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-rémail.nih.gov Email: cgapbs-rémail.nih.gov Tissue Procurement: DCTD/DTP/Cazdar Tissue Procurement: DCTD/DTP/Cazdar CDNA Library Preparation: Rubin Laboratory cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Lettlcia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lilsa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.	ion AUG-2 AUG-2 Cente	MGC. MGC. human. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2811)	iens ter) cds	.c 1776 	agaaagtgaaatggttcagatctgggaaaaaaacaagagactcaatggagacagaagaaa 1773 	accettttttecetgaaagtttgggaatgactettccagaaacettagagcagatgc 1713 	tacaacagaatgctgccctacatcgtcatgggtagtctgactgtc 	tcacatccacggcctccagagtgggcagcatcattgccccctactttgtttacctcggtg 1593 	

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                                             {\tt TCCTGCAGATCTTCTCGAAGAATTTTGAGATGTTTGTCGTGCTGTTTGTCCTTGTAGGCA}
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Qy 1144 tcaggactcggaatattgccataatgaccattatgtctttgctgctatggatgctgacct 1203		Db 323 GACAGGTGCCTCAGAAATGCCGCCGCTACCGACCATCGCCAACCTTCTCTGAGC 382 Qy 430 tcgggctggagccgggcgcgacctgggacctgggagcagcagcagagagag

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octn2; OCTN2.
Mus musculus
Mus musculus
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Submitted (24-JUN-1998) Jun-ichi Nezu, Chugai Research Institute
for Molecular Medicine, Inc., Gene Search Program; 153-2 Nagai,
Niihari, Ibaraki 300-4101, Japan (E-mail:nezuj@cimmed.com,
Tel:81-298-30-6211, Fax:81-298-30-6270)
Location/Qualifiers
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/dev_stage="adult"
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/codon_start=1
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            atatcatccaaaaagctgcaaaaatgaacaacacagctgtaccagcagtgatatttgatt
                                                                      ggttcattcctgaatctccccgatggctgatatcccagagaagatttagagagggctgaag
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                                                       GGTTCATCCCTGAGTCCCCACGATGGCTCATCTCTCAAGGCCGAATTAAAGAGGCAGAGG
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Mammalia; Eutheria; R
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AF110417
2 (bases 1 to 2621) Wu,X., Huang,W., Prasad,P.D., Conway,S.J. and Ganapathy,V.
                                                                                 Wu,X., Huang,W., Prasad,P.D., Seth,P., Rajan,D.P., Chen,J., Conway,S.J. and Ganapathy,V. Functional characteristics and tissue distribution organic cation transporter 2 (OCTNZ), an organic Ca
                                                     J. Pharmacol.
99384224
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            Rajan, D.P.,
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Query Match
Best Local Similarity
Matches 1246; Conserv
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caaccatggctgtacagactggcttcagcttcctgcagattttctccatcagctgggaga
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                                                                     TGGGCTCCTTCATTTCAGGACAGCTCTCAGACAGGTTTGGTCGCAAGAATGTGCTGTTTT
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Submitted (01-DEC-1998) Department of Biology, Medical College of Georgia, 30912-2100, USA
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/TEBHRCLVPHTVULSSAWRNHSIPLETENGGRQVPQKÇRRYRLATIANESELGLEPGRD
VDLEQLEGESCLDGWEYDKDVFLSTIVTEWDLVCKDÖWKAPLITISLFFVQLMGSFIS
GQLSDRFGRKNVLFLTMAMQTGFSFLQVFSVNESMFYVLFVLVGMGQISNYVAAFVLG
TEILSKSIRIFFATLGVGIFVARGFMYLLFLAYFIRDWRMLLLALTVPGVLCGALWWF
IPESPRKLISQGRIKEAEVIIRKAAKINGIVAPSTIRDWRMLLLALTVPGVLGALWWF
IPESPRKLISQGRIKEAEVIIRKAAKINGIVAPSTIRDWSELQDLNSTKPQLHHIYDL
IRTRNIRVITIMSIILWITISVGYFGLSLDTPNLHGDIYVNCFLLAAVEVPAVVLAWL
LLQYLPRRYSISAALFILGSSULLFMQLVPSELFYLLFYLLWGSLTILTAILTIL
ALLYPTVVRNMGVGVSSTASRLGSILSPYFVYLGAYÖRFLFYILMGSLTILTAILTILF
FPESFGVPLPDTIDOMLRVKGIKQWQISSQTRWQKDGBESPTVIKSTAF"
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/protein_id="AAD54060.1"
/db_xref="GI:5852406"
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                                                                           tgactcttccagaaaccttagagcagaatgcagaaagtgaaaatggttcagatctgggaaaa
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Query Match
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gacgccgcgaacctgagcagcgcctggcgcaacaacagtgtcccgctgcggctgcgggac
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2 (bases 1 to 3007)
Schomig, E., Spitzenberger, F.,
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Submitted (07-OCT-1997) D. (
Department of Pharmacology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus mRNA for putative integral membrane transport protein (UST2r).
AJ001933
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         /Codon_start=1
/product="putative integral membrane transport protein"
/protein_id="CAA05106.1"
/db_xref="G1:3004487"
/db_xref="G1:3004487"
/db_xref="SPTREMBL:070594"
/translation="MRDYDEVTAFLGEWGPFQRLIFFLLSASIIPNGFNGMSIVFLAG
/THENGLYPHTYNLSSAWNHSIPLETKNDGRQVPQSCRRYRLATIANFSALGLEPGRD
VDLEQLEQENCLDGWEYNKDVFLSTIVTEWDLVCKDDWKAPLTTSLFFVGVLMGSFIS
GOLSDRFGRKNVLFLTMGMQTGFSFLGLFSVNREMFTVLFVLVGMGGISNVVAAFVLG
TEILSKSIRIIFATLGVCIFYAFGFMVLPLFAYFIRDWRMLLLALTVPGVLCGALWWF
IPESFRWLISGGRVKEAEVIIRKAAKFNGIVAFSTIFDPSELQDLNSKKPQSHHYDL
VRTRNIRIITIMSIILWLTISVGYFGLSLDTPNLHGDIYVNCFLLAAVEVPAYVLAWL
LLQHLDRRYSISAALFLGGSVLLFIQLVPSELFYLSTALWVGKRGITSAYSMYVYT
AELYETVYRNMGVGVSSTASRLGSILSFYFVYLGAYDRFLPYILMGSLTILTAILTLF
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/db_xref="taxon:10116"
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Sciurognathi; Muridae; Murinae;
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e ro	ON Rattus norvegicus organic cation/carnitine transporter (OCTN2) mRNA, complete cds. N AF110416.1 GI:5852403 Norway rat. SM Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Mufidae; Murinae; Rattus Rattus, Drasad, P.D., Seth, P., Rajan, D.P., Leibach, F.H., Rattus, Conway, S.J. and Ganapathy, V. Functional characteristics and tissue distribution pattern of organic cation transporter 2 (OCTN2), an organic Cation/Carnitine transporter J. Pharmacol. Exp. Ther. 290 (3), 1482-1492 (1999) E 2 (bases 1 to 3037) E 2 (bases 1 to 3037) S Wu, X., Huang, W., Prasad, P.D., Rajan, D.P., Leibach, F.H., Chen, J., 19384228 D 10454528 D 10454528 D 2 (bases 1 to 3037) S Wu, X., Huang, W., Prasad, P.D., Rajan, D.P., Leibach, F.H., Chen, J., Direct Submission L Submitted (01-DEC-1998) Department of Biochemistry and Molecular Biology, Medical College of Georgia, 1120 15th Street, Augusta, G 30912-2100, USA	CTTCTCTTCATACAGCTGGTGCCTTCAGAATTGTTTACTTGTCCACTGCCCTGGT ctgggaaaatttgggatcacctctgctttctccatgctgtatgtcttcactgctga ctgggaaaatttgggatcacctctgctttctccatgctgtatgtcttcactgctga ctgGGCAAGTTTGGAATCACCTCTGCCTATTCCATGGTCTATGTTGTACACGGCCGA cacccaaccctggtcaggaacatggcggtgggggtcacatccacggcctccagagt

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LLQHLPRRYSISAALFLGGSVLLFIQLVPSELFYLSTALVNVGSGTTSAYSMYYVYT
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Direct Submission
Submitted (26-AUG-1998) Takashi Sekine,
of Medicine, Department of Pharmacology
Shinkawa, Mitaka, Tokyo 181, Japan (E-ma
                                                                                                          Rattus norvegicus
Eukaryota; Metazo
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  Japan (E-mail:QZV07422@nifty.ne.jp,
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               Kyorin University, School
and Toxicology; 6-20-2
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2 (sites)
Sekine,T., Kusuhara,H., Utsunomiya-Tate,N.,
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Molecular cloning and characterization
transporter from rat intestine
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="intestine"
/dev_stage="adult"
101__1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="CTI"
/codon_start=1
/product="high-affinity c
/protetn_id="BAA33399.1"
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TPEHRCLVPHTWILSSAWRNHSIPLERENGGROVPOSCRRYLLATIANTSALGLEGGR
VDLEGLEGENGLLGWERYKNDVELSTIVTEMDLLCKDDWARDLITSLEFFVOLMGSFIS
GOLSDREGRKNULFLINGMQTGFSFLOLFSVNIFEMFTVLFVLLVGMQGISNYVAAFVLG
TEILSKSIRIIFATLGVCIFYARGFMVLFLFAYFIRDMRHLLLALTVPCFULGAUNGF
IPESPRWLISGGRYKENEVIIRKAARENGIVARSTIFDPSELQDLNSKKPQSHHIYDL
VRTRNIRITIMSIILMLTISVGYFGLISLDFPNLHGDIYVNCFLAAVEVPAYVLAWL
LLQHLPRRYSISAALFLGGSVLLFIQLSLDFPLHGGITYNNCFLTAANTYVYTT
AELYFTVVRNWGVGVSSTASRLGSILSFYFVLGAYDRFLYILMGSLTITAAITITF
EPESFGAPLPDTIDQMLRVKGIKQWQLQSQTRTQKDGGESPTVLKSTAF"
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Molecular and Functional Characterization of Catlon/Carnitine Transporter Family in Mice J. Biol. Chem. 275 (51), 40064-40072 (2000)
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Genes homologous with organic cation transporters OCT1 and OCT2, useful in design of new drugs for treatment of diseases due to abnormality of the transporter functions

Claim 2; Page 45-51; 97pp; Japanese.

The present sequence encodes a protein with cation transporting activity. The genes are significantly homologous with organic cation transporters OCT1 and OCT2. The genes may used in drug development, particularly in the treatment of diseases due to abnormality of the organic cation transporter functions e.g. fatty liver, heart diseases and cancers, by controlling such as by inhibition or activation. Administration of anti-tumour and anticancer drugs in combination with a transporter protein inhibiting agent allows the agents to penetrate into the diseased cells to enhance the drug action.

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Administration of anti-tumour and anticancer drugs in combination with
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biplogical activity.
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                gaaaaaaacaagagactcaatggagacagaagaaaatc
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RESULT
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Key
                             Organic cation heart disease;
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               musculus
                                                  encoding a
                                                                                               standard;
                                                                  (first
                            transporter; OCT1; OCT2;
cancer; anti-tumour drug
                                                   protein with cation transporting
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                           atggctgggagtacgacaaggacgtcttcctgtccaccatcgtgacagagtgggacctgg
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protein (OCTN3). Also describes a mouse organic cation transporter protein (OCTN3). Also described are: (1) a method for screening compounds for their ability to regulate the transport of an organic cation into the cell, by generating a cell expressing OCTN3 at the cell membrane, contacting with the compound and organic cation, and observing the degree of transport of the organic cation, and
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                                                                                                                                                                                                                                                                                                                            Systemic carnitine deficiency cation transporter, useful as
                                                                                                                                                                                                  Sequence
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                                                           tctgtgggcctctgagggcggcatgcgggactacgacgaggtgaccgccttcctgggcga
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                                                                                                                                                                                                                         The present invention describes a method for detecting the presence polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to contain the colitis and Crohn's disease.
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                                                                        the presence of genetic polymorphisms associated with inflammatory disease and correlating their occurrence with disease states. They used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a goot containing a polymorphic site described in the exemplification of the present sequence.
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                              used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a containing a polymorphic site described in the exemplification of
                                                                polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to determine the presence of genetic polymorphisms associated with inflammatory bower disease and correlating their occurrence with disease states. They may
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                                                                                                                                       Disclosure;
                                                                                                                                                            Testing for the presence of polymorphisms associated bowel disease, using a hybridization assay -
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                                                                                                                 The present invention describes a method for detecting
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Search completed: July 17, 2002, 01:51:58 Job time: 18884 sec

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: O'Connor, Steven P
                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/040,444 FILING DATE: March 18, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
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Gorboulev, Valentin
GORDOULEV, Valentin
WENTION: Transport protein Which Effects The
WENTION: Transport Of Cationic Xenobiotics and\or Pharmaceuticals,
WENTION: DNA Sequences Encoding It And Their Use.
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Best Local :
                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Toohey Kimberlin M
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02481.1453-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1882 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE:
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COUNTRY:
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GENERAL INFORMATION:

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US-09-040-444-4
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Best Local Similarity
Matches 585; Conserv
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APPLICANT: Gorboulev
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: 2481.1453-01
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CITY: Washington
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Gorboulev, Valentin
Gorboulev, Valentin
VENTION: Transport protein Which Effects The
VENTION: Transport Of Cationic Xenobiotics and/or
VENTION: DNA Sequences Encoding It And Their Use.
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Pred. No. 1.3e-36;
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RESULT 5
US-08-01-572-5
; Sequence 5, Application US/08501572
; Patent No. 6063623
; GENERAL INFORMATION:
APPLICANT: KOEPSell, Hermann
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APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport (
TITLE OF INVENTION: Transport (
TITLE OF INVENTION: DNA Sequend
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                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
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Matches 612; Conserv
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1885 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
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ATTORNEY/AGENT INFORMATION:
NAME: Toohey, Kimberlin
REGISTRATION NUMBER: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acctggggcagctggagcaggagagctgcctggatggctgggagttcagccaggacgtct 516
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                                                                                                                       CCCTGCCCACCTTCCTCCTCCTGCTCTACTACTGGTGTGCCGGAGTCCCCTCGGTGGC
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                                         TGTTATCACAAAAAGAAACACTGAAGCAATAAAGATAATGGACCACATCGCTCAAAAGA
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Patent No. 6063766
GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                     STREET: 1300 I SCATTY: Washington STATE: D.C. COUNTRY: COUNTRY: USA ZIP: 20005-3315
                ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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   CURRENT APPLICATION DATA:
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                                                                                                                                                                E: Finnegan, Henderson, Farabow, Garrett &
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                Koepsell, Hermann Grundeman, Dirk Grundeman, Dirk Gorboulev, Valentin Which Effects The NVENTION: Transport protein Which Effects The NVENTION: Transport Of Cationic Xenobiotics and or Pharmaceuticals, NVENTION: DNA Sequences Encoding It And Their Use.

SEQUENCES: 6
                   Version
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Best Local Similarity 48.4%;
Matches 612; Conservative
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TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1885 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
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NAME: O'Connor, Steven F
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tgtctttgctgctatggatgctgacctcagtgggttactttgctctgtctctggatgctc 1236
                                 agcagaaagctttcattctggacctgttcaggactcggaatattgccataatgaccatta 1176
                                                                                                  ATGGGAAGTTGCCTCCTGCTGATTTAAAGATGCTTTCCCTCGAAGAGGATGTCACCGAAA 1057
                                                                                                                             acaacacagctgtaccagcagtgatatttgattctgtggaggagctaaatcccctgaagc 1116
                                                                                                                                                                  TGTTATCACAAAAAAGAAACACTGAAGCAATAAAGATAATGGACCACATCGCTCAAAAGA
                                                                                                                                                                                    tgatatcccagagaagatttagagaggctgaagatatcatccaaaaaagctgcaaaaaatga
                                                                                                                                                                                                                                 CCCTGCCCACCTTCCTCTTCCTGCTCTACTACTGCTGTGTGCCGGAGTCCCCTCGGTGGC
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Patent No. 5972702
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walf
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APPLICANT: Brady, F
TITLE OF INVENTION:
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                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                         ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7048
              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                               STREET: 600 A:
CITY: Boston
STATE: MA
                                                                                                                      CLASSIFICATION:
                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 02210
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Best Local Similarity
Matches 538; Conserv
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LENGTH: 2102 base pairs
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HYPOTHETICAL:
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STRANDEDNESS: double
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                                                                             aatgaccattatgtctttgctgctatggatgctgacctcagtgggttactttgctctgtc 1225
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 TATGGGAGTAGAAGAATTTGGAGTCAACATCTACATACTCCAGATCATCTTCGGTGGGGT 1213
               CACCTCAGCCAAGGTCAAATATGGCTTATCTGACTTGTTCCGAGTGTCCATCCTGCGCCG
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                                                                                                         NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 108, Application US/08592126 Patent No. 5821091 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1334
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
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                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 370 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gregory Dolganov
                                                    TYPE: nucleic acid
                                  STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cctcggtgcttacaacagaatgctgccctacatcgtcatgggtagtctgactgtcctgat 1645
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                  linear
cDNA to mRNA
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                                                                                                                                                                                                                                                                                                     us/08/592,126
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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE:
US-08-592-126-108
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Query Match 4.9
Best Local Similarity 76.3
Matches 128; Conservative
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 105
SECURENCE CONTROL TO THE PARTY CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     HYPOTHETICAL: N
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 481 base pairs
TYPE: nucleic acid
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NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
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                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1: MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 CAGGTTTGGCCGGAAGAATGTGCTGTTCGTGACCATGGGCGTGCAGACAGGCTTCAGCTT 162
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                          INDIVIDUAL ISOLATE:
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128; Conser
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151
                           4.9%;
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Score 104; DB 1;
Pred. No. 3.8e-18;
0; Mismatches 4(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4600-0111
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   40;
                                                         Length 481;
Indels
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Gaps
0;
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PCT-US95-14418-3
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LOCATION:
PCT-US95-14418-3
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                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 184; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1794 base pairs
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                      187
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                                                                                                                          404
 524
                                                             464
                                                                                            247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 :
CITY: Chicago
                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
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                                                                                                                         GGGACGACCCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACCACCCCCGAGGGGG
                                                                                                                                                     gggggcccttccagcgcctcatcttcttcctgctcagcgccagcatcatccccaatggct 246
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AGAGGCTCCATCGGAACCTCCTTAAGCGCCTCGAGGGGGAGGAGAAGCTCCTTTGGCTCT
                        acgccgcgaacctgagcagcgcctggcgcaacaacagtgtcccgctgcggctgcgggacg
                                                             tcaatggtatgtcagtcgtgttcctggcggggaccccggagcaccgctgtcgagtgccgg 306
                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Illinois
                                                                                                                                                                                                                                                                                                                                                                                           1794 base pairs
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                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                       2.6%;
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                                                                                                                                                                                                     Score 55; DB 5; Pred. No. 7.5e-05;
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                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                        215;
                                                                                                                                                                                                                     Length 1794;
                                                                                                                                                                                        Indels
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GENERAL INFORMATION:
                                                                                                                              Matches
                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                247
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TOPOLOGY: linear
                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                           LENGTH: 1794 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gass, David A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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TGGCGCGGCGCTACGGGGGGGAGTGGACGGAGGACGCCGCCCACCGGGCCCTCCTCTCGG
                                                             GGGACGACCCCATGCTCCTCCTACCTCCTGGACCCCCTCCAACACCACCCCCGAGGGGG 463
                                                                                 gggggcccttccagcgcctcatcttcttcctgctcagcgccagcatcatccccaatggct 246
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                    tcaatggtatgtcagtcgtgttcctggcggggaccccggagcaccgctgtcgagtgccgg 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGAGGAGGAGGTCTTCCGCTTGGCGGGCCACCCCTTCAACCTCCAACTCCCGGGACCAGC
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                                                                                                                              184;
                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                              Conservative
                                                                                                                                                                                                                                               CDS
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                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                            single
                                                                                                                                             2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biologically Active Fragments Thermus Flavus DNA Polymerase
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Power, 233
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                                                                                                                            Score 55; DB 5
Pred. No. 7.5e-
0; Mismatches
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South Wacker Drive
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                                                                                                                            DB 5; Le
7.5e-05;
hes 215;
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PCT-US95-14418-1
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PCT-US95-14418-1
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                                                                 Matches
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Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
1415 GGGACGACCCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACCACCCCCGAGGGGG 1474
                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                              MOLECULE TYPE:
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NUMBER OF SEQUENCES:
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                  187 99999cccttccagcgcctcatcttcttcctgctcagcgccagcatcatcccccaatggct 246
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                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                          3048 base pairs
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                                                              2.6%;
ilarity 46.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                             CDS
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                                                                                                                                                                                                                                         single
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                                                                                                                                                                                                                                                                                                                                                                                        28003/32330
                                                            Score 55; DB 5; Pred. No. 0.0001; 0; Mismatches 21:
                                                              215;
                                                                                           Length 3048,
                                                              Indels
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PCT-US95-15327-1
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Query Match 2.6%;
Best Local Similarity 46.1%;
Matches 184; Conservative
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                                                                                                                                                                                                                                                                    TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3048 base pair
                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Too
STREET: 6300 Sears Tower,
                                                                                                                                               FEATURE:
                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                          NAME/KEY:
                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                             LENGTH: 3048 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 38 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                           LOCATION:
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312/474-0448
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Thermus Flavus DNA F
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Score 55; DB 5; Pred. No. 0.0001; 0; Mismatches 21

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                  SOFTWARE: WOR'D PETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6
FILING DATE:
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                NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                          ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Moffett, R. Bru
APPLICANT: Fuller, Carl W.
TITLE OF INVENTION: THERMO
TITLE OF INVENTION: POLYME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                         FILING DATE: May 31, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
SEQUENCE CHARACTERISTICS:
                                                                          TELECOMMUNICATION INFORMATION:
                     TELEFAX: (2-
TELEFAX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                   REGISTRATION NUMBER: 32,327
                                                             TELEPHONE:
                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                       APPLICATION NUMBER:
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                                            (213) 489-1600
213) 955-0440
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US-08-073-384C-3
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Best Local Similarity
Matches 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08073384C Patent No. 5541311
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    APPLICANT: Lyamichev APPLICANT: Brow, Mai TiTLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/986,330
                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                 COMPUTER READABLE FORM:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                              STREET: 220 Francisco
                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         APPLICATION NUMBER: US/0 FILING DATE: 04-JUN-1993
                                                                                                      SOFTWARE:
                                                                                                                                                                                              COUNTRY:
APPLICATION NUMBER: US 0 FILING DATE: 07-DEC-1992
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VENTION: SYNTHESIS-DEFICIENT THERMOSTABLE

VENTION: POLYMERASE
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Lyamichev, Victor I.
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ATTORNEY/AGENT INFORMATION:

NAME: CAITOIL, Peter G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-00613

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/705-8410

TELEPHONE: 415/705-8410

TELEPHONE: 415/909-8338

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2504 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

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1475 TGGAAAGGGTGCTCTTTGACGAGCTTAGGCTTCCCGCCT 1513
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Search completed: July 16, 2002, 23:48:24 Job time: 13255 sec

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Minimum DB
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BG870249 602791116
AA428995 zv48b07.r
BG332869 602430714
BI647860 603276129
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16.3	16.4	16.5	16.6	17.2	17.5	17.5	17.5	17.8	17.8	17.8	18.0	18.1	18.4	18.4	18.5	19.1	19.3			19.4							
371	606	371	377	456	762	484	482	866	922	403	402	556	605	522	645	426	839	514	689	442	640	641	917	433	846	806	507
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prime, mRNA sequence.
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Db 381 GGGACGG Qy 421 tctcggc	Db 321 TGCCGGA Qy 361 gggacgg	Db 261 ATGGCTTG Qy 301 tgccgga	Db 201 GCGAGTK	Db 141 CAAGTY Qy 181 gcgagt	Db 81 CTTGGGG Qy 121 caagttt	Db 21 ccccgcc Qy 61 cttgggg	881	Query Match Best Local Simi	BASE COUNT ORIGIN				FEATURES Source	COMMENT Contact Genos Bp 19	REFERENCE 1 (A. AUTHORS Li, W. TITLE Full-	MS	DEFINITION AL557 Prime ACCESSION AL557 VERSION AL557 VERSION AL557

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Contact: Robert Strausberg, Ph.D.
Email: Capabs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM11691 row: p column: 13
High quality sequence stop: 671.
Location/Qualifiers
                                                          gccgcgaacctgagcagcgctggcgcaacaacagtgtcccgctgcggctgcgggacggc 368
                                                                                                                                                                                               aatggtatgtcagtcgtgttcctggcggggaccccggagcaccgctgtcgagtgccggac 308
                                                                           cgcgaggtgccccacagctgcagccgctaccggctcgccaccatcgccaacttctcggcg
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 910)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:5274108"
/clone_lib="NIH_MGC_95"
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/db_xref="taxon:9606"
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OUNT 15	JOURNAL Unpublic COMMENT Contact Email: This circle Insert Seq print Seq pri	X X	RESULT 5 AI032763/C LOCUS AI032763 DEFINITION 0x13h02.x: Clone IMAC CACCESSION AI032763 VERSION AI032763 KEYWORDS EST.	Qy 789 tt 790 l Db 665 AT 666	Qy 729 atgttcac Db 605 ATGTTTGT	Qy 669 gcaaccat Db 545 GTGACCAT	Qy 609 ctcggctc 	Qy 549 gtgtgtg:	Qy 489 gatggcts
rganism="Homo sapiens" b.xref="taxon:9606" lone="IMAGE:1656243" lone=lib="Soares_fetal_liver_spleen ex="made" ev_stage="20 week-post conception for the spleen polylinker; Site_l: play hamodified polylinker; Site_l: play hamodified polylinker; Site_l: play hamodified polylinker; Site_l: play is a subtracted version of the over spleen INFLS library. 1st strath a pac I - oligo(dT) primer [5] corrected constant packed to Enharmacia), digested with pac I and of Eco RI sites of the modified pTTInt through one round of normalization structed by Bento Soares and M.Fatinstructed by Bento Soares and M.Fatinstructed by Bento Soares and M.Fatinstructed by Bento Soares	ished (1997) ished (1997) ished (1997) cropapts refmail.nih.gov cropapts refmail.nih.gov cone is available royalty-free through consortium (info@image.llnl.gov) for 1 Length: 1014 Std Error: 0.00 length: 40ml3 fwd. ET from Amersham mality sequence stop: 353. Location/Qualifiers 1.559	MAT LE B	559 bp mRNA 111 Scares_fetal_liver_spleen_lNFLS_S1 3E:1656243 3' similar to TR:014946 0: ATION TRANSPORTER. ;, mRNA sequence		atgttcactgtgttatttgtcatcgtgggcatgggccagatctccaactatgtggtagcc 	caaccatggctgtacagactggcttcagcttcctgcagattttctccatcagctgggag TGACCATGGGCATGCAGACAGGCTTCAGCTTCCTGCAGATCTTCTCGAAGAATTTTGAG	<pre>ctcggctccttcgtgtccgggcagctgtcagacaggttttggcaggaadaacgttctcttc</pre>	gtgtgtgaggacaactggaaggtgcccctcaccacctccctgttcttc; 	galggetgggagtteageeaggaegtetaeetgteeaeegtegtgae¢gagtggaatetg
_INFLS_S1" Color	LLNL ; contact the further information.	nidae; Euteleostomi; nidae; Homo. ny Project (CGAP),	ear EST 28-AUG-1998 Homo sapiens cDNA 14546 POLYSPECIFIC		tatgtggtagcc 788 TATGTGGCAGCC 664	atcagctgggag 728 	aacgttctcttc 668 AATGTGCTGTTC 544	gtaggcgtgctc 608 GTGGGTGTGCTG 484	gagtggaatctg 548 GAGTGGAACCTG 424

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                                                                                                                                                                                                                                                                                                                                                                                     AW264315 613 bp mRNA linear xq98b08.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone similar to TR:014546 014546 POLYSPECIFIC ORAGANIC
                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

1 (bases 1 to 613)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurola

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)
                                                                          Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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AW264315.1 GI:6641057
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                Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Pred. No. 3.9e-104;
0; Mismatches 7;
 Gibco
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            Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Rodentia; Sciurognathi; M
1 (bases 1 to 577)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                               Mus musculus
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AW476024.1
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                                                                              house mouse
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Site_2: NotI; Cloned unidirectionally. Primer:
Library constructed by Life Technologies."
a 112 c 133 g 205 t
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/Clone_lib="NCI_CGAP_Brn53"
/tissue_type="three pooled |
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ity sequence stop: .
Location/Qualifiers
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Institute,
                                     Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae;
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                          TGACTGTAACGATTGACACCAAAATGAACCTTGCTATCAAGAAATGCTCGTCATACAGTA
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                                                                                                                                                                                                                                                                                                                                                                                    534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Other_ESTs: uq83d03.yl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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/strain="CZECH II"
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Pred. No. 6.3e-101;
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the through contact the contact the contact through contact the contact through                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW592711 544 bp mkNA L1 hf46606.x1 Soares_NFL_T_GBC_S1 Homo sapiens c IMAGE:2934946 3' similar to TR:014546 014546
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Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Benaldo. "
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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A1628726.1
                                                                                                                                                                                                                                 www-bio.lln1.gov/bbrp/image/image.html
Insert Length: 595 Std Error: 0.00
Seq primer: -40Up from Gibco
High quality sequence stop: 455
                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1628726 498 bp mRNA linear ty78b05.x1 NCI_CGAP_Kidl1 Homo sapiens cDNA clone similar to TR:014546 014546 POLYSPECIFIC ORAGANIC
                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
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National Cancer Institute, Cancer Genome Ana
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with. a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library
                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:2285169"
/clone_lib="NCI_CGAP_Kidll"
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Email: Capabs remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Schiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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1 (bases 1 to 611)
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/db_xref="taxon:9606"
/clone="IMAGE:4829882"
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/lab_host="DH10B"
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10842 row: o column: 03
High quality sequence stop: 708.
                                       tgaggacaactggaaggtgcccctcaccacctccctgttcttcgtaggcgtgctcctcgg
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Mammalia; Eutheria; Rodentia; SC
1 (bases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/.
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/db_xref="taxon:10090"
/clone="IMAGE:4922714"
/clone_lib="NCI_CGAP_SG2"
/clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B (T1 phage-resistant)"
/note="organ: salivary gland; Vector: pcMV-SPORT6; Site
/note="organ:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ∕organism="Mus musculus"
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470 bp mRNA linear EST 16-OCT-
2v48b07.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone
LNAGE:5756853 5' similar to TR:G1293672 G1293672 KIDNEY-SPECIFIC
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1 (bases 1 to 470)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
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Eukaryota; M
                                                                                                                                                                                                                                                                                                                                                               Washington University Sche 4444 Forest Park Parkway, Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
TMAGE Consortium (info@inage.llnl.gov) for further:
Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-Merck EST Project 1997
                103
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314 286 1810
          /clone="IMAGE:756853"
/clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                        /sex="Female"
                                                                                                                                                                                                                                   /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail:nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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BG332869.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                                                                        Plate: LLCM1238 row: k column: High quality sequence stop: 741.
                                                                                                                                                                                  found through the I.M.A.G.E. http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                    CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 754)
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/OIYGHILDM

/OLDARDEF TEXON:9606"

/Clone_fib="NIH_MGC_18"

/Clone_lib="NIH_MGC_18"

/tissue_type="large coll carcinoma"

/tab_host="DH10B (phage-resistant)"

/lab_host="DH10B (phage-resistant)"

/lab_hordan: lung; Vector: pOTB7; Site_1: XhoI;
                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:13139307
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Pred. No. 9.
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                                                                                                         mRNA sequence.
BI647860
BI647860.1 GI
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 799)
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603276129F1 NIH_CGAP_Mam3
                                                     Mus musculus
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                                                                                                             GI:15562096
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nes 582; Conserv
                                                                             9t9t9cacattttttgcagttggctatatgctgctgccactg-tttgcttacttcatcag
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11802 row: i column: 08
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Tissue Procurement: Lothar Hennighausen
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan
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nilarity 79.58;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="tumor, gross tissue"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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ggcggatgctgctgctggcgctgacggtgccgggagtgctgtgtgtcccgctgtggtggt 972
                                GCACATTTTTTGCAATTGGCTACATGCTGCTGCCACTGTTTGCTTACTTCATCATAGACT 63
                                                 GGTGATCATCCCGCAAAAGCTGCAAAAATCAATGGGATTGTTGCACCTTCCACTATCTTC
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                                                                                          tch 20.5%; al Similarity 86.6%; 497; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases c
v0.980904.e. Vector identified
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Sonstegard TS
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research
Belg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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232219 BARC 5BOV Bos taurus
BE846144
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FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                       Seq
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                                                                                                                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."
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                                                                                        Score 438.4; DB 10;
Pred. No. 1.5e-84;
0; Mismatches 71;
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            tcattcaactggtacctgtggattattacttctt 1420
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Search completed: July 16, 2002, 21:46:42 Job time: 7978 sec

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Drosophila melanog	Rat organic anion	hOAT1. Homo sapie	Human organic anio	Mouse organic anio	Drosophila melanog	Drosophila melanog	001	Rat cerebral organ	Hydrophobic domain	Human protein havi	Human osteoclast t	Human transporter	an	hOAT3. Homo sapie	Human liver-specif	A human organic an	erebra.	hOAT2A. Homo sapi	Ξ	*	a melan	Rat liver anion tr	æ	prote	liver	human		ein SEQ		bone	Human ORFX ORF2802	O .	Drosophila melanog

ALIGNMENTS

23-JUN-1999 (first entry)

AAY01650;

AAY01650 standard; Protein;

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AV Gene A protein with cation transporting activity. 20-MAY-1998; 08-SEP-1997; 07-SEP-1998; WO9913072-A1 Homo sapiens Organic cation transporter; OCT1; OCT2; drug development; fatty liver; heart disease; cancer; anti-tumour drug; anticancer drug. WPI; 1999-215062/18. Nezu J, Oku A; 18-MAR-1999. N-PSDB; (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC AAX26880 98JP-0156660. 97JP-0260972. 98WO-JP04009

Genes homologous with organic cation transporters OCT1 and OCT2, useful in design of new drugs for treatment of diseases due to abnormality of the transporter functions

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       Organic cation transportation; human; OCTN2; diagnosis; systemic carnitine;
                             Human carnitine
                                                         AAY83929;
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This sequence represents the human carnitine transporter protein OCTN2 The coding sequence can be used as a target for diagnosis of systemic carnitine deficiency by detecting the presence of mutations in the sequence, especially seen in the disease juvenile visceral steatosis (jvs). The wild type OCTN2 gene can be used in the gene therapy of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease state.
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                                                                                     AKANGIVVPSTIFDPSELQDLSSKKQQSHNILDLLRTWNIRMYTIMS]MLMMTISVGYFG
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Similarity 100.0%;
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Pred. No. 0;
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RESULT ARBOJOLS ID ARGONOLS ACC ARGONOLS ACC ARGONOLS ARGONOLS ACC ARGONOLS                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and C polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The C polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC in restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fig. wipo.int/pub/published_pct_sequences.
Query Match
Best Local Similarity
Matches 557; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess responsible for genetic disorders or other traits.
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder.
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N-PSDB; AAX26902.
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08-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A protein with cation transporting activity.
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  Genes homologous with organic cation transporters OCT1 and OCT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Organic cation transporter; OCT1; OCT2; drug development; fatty liver; heart disease; cancer; anti-tumour drug; anticancer drug.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Administration of anti-tumour and anticancer drugs in combination with a transporter protein inhibiting agent allows the agents to penetrate into the diseased cells to enhance the drug action.
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         Mouse OCTN2
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                                                                                                                                                  VYLGAYDRFLPYILMGSLTILTAILTLFLPESFGTPLPDTIDQMLRVKGMKHRKTPSHTR
                                                                                                                                                                       {\tt pselfylstalvmvgkfgitsaysmvyvytaelyptvvrnmgvgvsstasrlgsilspyf}
                                                                                                                                                                                PPDLYYLATVLVMVGKFGVTAAFSMVYVYTAELYPTVVRNMGVGVSSSTASRLGSILSPYF
                                                                                                                                                                                                                 LSLDTPNLHGDIFVNCFLSAMVEVPAYVLAWLLLQYLPRRYSMATALFLGGSVLLEMQLV
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No. 5e-264;
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Query Match
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Matches 476
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AKANGIVVPSTIFDPSELQDLSSKKQQSHNILDLLRTWNIRMVTIMSLMLWMTISVGYFG
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Pred. No. 5e
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Best Local Similarity
Matches 476; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the mouse carnitine transporter protein OCTN2. The coding sequence of the corresponding human protein can be used as a target for diagnosis of systemic carnitine deficiency by detecting the presence of mutations in the sequence, especially seen in the disease juvenile visceral steatosis (jvs). The wild type OCTN2 gene can be used in the gene therapy of the disease state.
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organic cation transportation; mouse; OCTN2; diagnosis; systemic carnitine juvenile visceral steatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 47-51; 106pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Systemic carnitine deficiency cation transporter, useful as
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QDVYLSTIVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRKNVLFVTMGMQ
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Pred. No. 5e-264;
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deficiency; mutation; gene ther
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                                                                                                                                                                                  Organic cation transporter gene OCTN3 expressed in testis for identification of regulators of carnitine transport for use a
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fication; regulator;
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                                                                                                                                              Page 34-39; 58pp; Japanese.
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The present invention describes a mouse organic cation transporter protein (OCTN3). Also described are: (1) a method for screening compounds for their ability to regulate the transport of an organic cation into the cell, by generating a cell expressing OCTN3 at the cell membrane, contacting with the compound and organic cation, and observing the degree of transport of the organic cation; and (2) a

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Best Local Similarity 80.6
Matches 435; Conservative
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                                                                                          Organic cation heart disease;
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           07-SEP-1998;
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                                                                                          transporter; OCT1; OCT2; drug development; cancer; anti-tumour drug; anticancer drug.
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08-SEP-1997;
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                                       VYLGAYDRELPYILMGSLTILTAILTLELPESFGTPLPDTIDQMLRVKGMKHRKTPSHTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes homologous with organic cation transporters OCT1 and OCT2, useful in design of new drugs for treatment of diseases due to abnormality of the transporter functions
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08-SEP-1997;
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97JP-0260972.
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72.2%;
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Pred. No. 2.5e-224;
67; Mismatches 84;
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                                 The present invention describes a mouse organic cation transporter protein (OCTN3). Also described are: (1) a method for screening compounds for their ability to regulate the transport of an organic cation into the cell, by generating a cell expressing OCTN3 at the cell membrane, contacting with the compound and organic cation, and observing the degree of transport of the organic cation, and observing the degree of transport of the cyanic cation, and the cell by OCTN3, by generating a cell expressing OCTN3 at the cell membrane, contacting with the compound and observing the degree of transport of the compound. OCTN3 can be used for the identification of regulators of the transport of organic cations (especially carnitine) into cells by OCTN3, for use as drugs. The present sequence represents the mouse OCTN1 amino acid sequence, which is used in an example from
                                                                                                                                                                                                                                                          Organic cation identification
                                                                                                                                                                                                                                                                                                                                Nezu
                         the present invention
                                                                                                                                                                                                                                Example 2; Fig 2; 58pp; Japanese.
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carnitine transport
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                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 13629
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11-JUL-2000;
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Pred. No. 2.5e-224;
57; Mismatches 84;
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ed----genfgkkpapqetaeeg
                                                glgassmvarvggilapylkllgeiwrplpliicgaisttagllsil:
                                                                   GVGVSSTASRLGSILSPYFVYLGAYDRFLPYILMGSLTILTAILTLFLPESFGTPLPDTI
                                                                                                         rkdeafviiekaakenkvevpneiyeqlvdevaekkkqdemaasqpaatvfdllrypnlr
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                          DQMLRVKGMKHRKTPSHTRMLKDG
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Pred. No. 5.7e-87;
)6; Mismatches 206;
534
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genes from Drosophila
interactions -
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ifvmmffsvgfmltavfayfvhdwrwlqialtlpglifmfyywiipesarwlllkgrkdc
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Pred. No. 1.9e
21; Mismatches
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No. 1.9e-79;
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20-OCT-2000;
30-NOV-2000;
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19-JUL-2000;
01-SEP-2000;
                                                                                                                                                 Tang YT,
Zhao QA,
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27-APR-2000;
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                                                                              Nucleic acids encoding polypeptides with cytokine-like useful in diagnosis and gene therapy -
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N-PSDB; AAK51500.
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Wang D,
Yang Y,
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2000US-0560875
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Wejhrman T,
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Zhang J, Ren
T, Goodrich R
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R, Wang
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or

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                       vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                      Human; open reading
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Pred. No. 5.8e
10; Mismatches
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                                                                                        detection;
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                                                                   cytostatic; hepatotropic; nootropic; neuroprotective;
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which represent the human ORFX open reading frames 1 to 3161. The ORFX contributions and partitions such as cytostatic, hepatotropic; vulnerary; contributions have activities such as cytostatic, hepatotropic; vulnerary; cantipsoriatic; antiparkinsonian; nootropic; neuroprotective; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; antiparkinsonian; nootropic; immunosuppressant; antiparkinsonian; thrombolytic; coagulant; vasotropic; cantidiabetic; hypotensive; dermatological; immunosuppressive; antiparkinson; and antiparkinson; antipological; antithrematic; cantithyroid; and antiparentic. The sequences can be used for determining contributions and antiparentic to, or preventing or treating contributions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy contributed disorders, neurodegenerative disorders, osteoarthritis, corrections in hypothyroidism, cholesterol ester storage, systemic lupus carythematosus, severe combined immunodeficiency (SCID), AIDS, virial, contributed immuno autoimmune disorders. Asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobhnuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 4791-4792; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
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                                                           erythematosus, severe combined immunodeficiency (SCII bacterial or fungal infection, malaria, autoimmune di allergies, aplastic anaemia, burns, wounds, bone and nocturnal haemoglobinuria, antiinflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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Sequence
                                     coagulation; to inhibit thrombosis;
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99US-0127636.
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Query Match Best Local :

Similarity

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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
30-NOV-2000;
                  Ford JE, Boyle BJ, Tang YT, I
Ren F, Wang J, Werhman T, Xu
Zhao QA, Zhou P, Drmanac RT;
                                                                                                                                                                                                                                                                                                      Human; bone marrow; antiinflammatory; cytostatic; neuroprotec antiviral; antibacterial; antifungal; anti-HTV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cell differentiation modulator;
                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001
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                                                                                                                                                                                                                                                                                              immunodeficiency
                                                                    HYSEQ INC
                                                                                                               2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0653451.
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2000US-0250583
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                                  Liu C, Xue
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                                Chen Y, Z
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Best Local Similarity
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etlgkrlattweeaaklesenesks
                                      ESFGTPLPDTIDQMLRVKGMKHRKT
                                                                       \verb|aelyptivrslavgsgsmvcrlasilapfsvdlssiwifipqlfvgtmallsgvltlklp|
                                                                                                              AELYPTVVRNMGVGVSSTASRLGSILSPYFVYLGAYDRFLPYILMGSLTILTAILTLFLP
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No. 6e-76;
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Search completed: July 17, 2002, Job time: 8148 sec

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Minimum DB
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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   231628 seqs, 24425594 residues
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-040-444-1
US-09-040-444-2
US-08-964-127-2
US-09-031-392-5
US-09-031-392-5
US-09-031-392-10
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US-09-031-392-10
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 Sequence 3, Patent No. (
 TELEFAX: (202)408-4400 INFORMATION FOR SEQ ID NO:
 GENERAL INFORMATION:
 APPLICANT:
APPLICANT:
 SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,44
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SEQUENCE
 TELECOMMUNICATION INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION: TITLE OF INVENTION:
 471
 356
 298
 238
 234
 181
 174
 123
 114
 292
 NAME: O'Connor, Steven P
REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 24
 FILING DATE: M
CLASSIFICATION:
 TELEPHONE:
 COUNTRY:
 STREET:
 ADDRESSEE:
 63
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 , Application US/09040444 6063766
 20005-3315
 Washington
CHARACTERISTICS:
 D.C
 E: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
1300 I Street, N.W., Suite 700
 Grundeman, Dirk
Gorboulev, Valentin
Gorboulev, Valentin
WENTION: Transport protein Which Effects The
WENTION: Transport of Cationic Xenobiotics and or Pharmaceuticals,
WENTION: DA Sequences Encoding It And Their Use.
 USA
 Koepsell, Hermann
 (202)408-4000
 March 18, 1998
 US/09/040,444
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 Version
 #1.30
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 US-08-501-572-1
 Patent No. 6063623
 Sequence 1,
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Best Local
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
 GENERAL INFORMATION:
 APPLICANT: Gorboulev
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
 APPLICANT:
 APPLICANT:
 475 DIGGIITPFLYYRLTNIWLELPLMYFGYLGLYAGGLALLLPETKGKALPETIEE
 356 FTSSVLYQGLIMHM-GLAGDNIYLDFFYSALVEFPAAFMIILIIDRIGRRYPWAASNMVA
 181 LTTVLINAAAGVLMAISPTYTWMLIFRLIQGLVSKAGWLIGYILITEFVGGRYR----RTV
 Local Simhes 187;
 STATE:
 CITY: Washington
 STREET:
 ADDRESSEE:
 63 CGWSPAEELNYTVPGPGPAGEASPRQCRRYEVDWNQSTFDCVDPLASLDTNRSRLPLGPC
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 RDGWYY - - ETPGSSIVTEFNLVCANSWMLDLFQSSVNVGFFIGSMSICYIADRFGRKLCL
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 DDVLEHGGEFHFFQKQMFFLLALLSATFAPI-YVGI--VFLGFTPDHRCRSPGVAELSLR
 D.C.
 Similarity
 Application
 1300 I Street,
 555
 Gorboulev, Valentin
 Grundeman, Dirk
 Koepsell, Hermann
 Conservative
 Finnegan, Henderson, Farabow, Garrett 00 I Street, N.W., Suite 700
 amino acids
 peptide
 single
 Transport protein Which Effects The Transport Of Cationic Xenobiotics and\or Pharmaceuticals DNA Sequences Encoding It And Their Use.
 25.2%;
 US/08501572
 98;
 Score 726; DB 3;
Pred. No. 5.9e-68;
 Mismatches
 Version
 #1.30
 Length
 δ.
 Indels
 528
 Gaps
 414
 410
 180
 173
 474
 470
 355
 351
 297
 291
 237
 122
 62
 233
 14;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE:

US/08/501,572

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RESULT 4
US-09-040-444-1
Sequence 1, Application US/09040444
Patent No. 6063766
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 US-08-501-572-1
 Query Match
Best Local :
 Matches
 GENERAL INFORMATION:
 TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 NAME: Toohey Kimberlin M
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02481.1453-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-44000
 STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
 APPLICANT:
 ATTORNEY/AGENT INFORMATION:
 458
 454
 398
 394
 338
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 280
 274 WWFIPESPRWLISQGRFEEAEVIIRKAAKANGIVVPSTIFDPSELQDLSSKKQQSHNILD
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 58
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 1 MPTVDDVLEQVGEFGWFQKQAFLLLCLISASLAPI-YVGI--VFLGFTPGHYCQNPGVAE
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 1 MRDYDEVTAFLGEWGPFQRLIFFLL---SASIIPNGFTGLSSVFLIATPEHRCRVPDAAN 57
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 194;
 Similarity
 amino acid
 556 amino acids
Koepsell, Hermann
Grundeman, Dirk
 Conservative
 ------CEHGWVY--DTPGSSIVTEFNLVCGDAWKVDLFQSCVNLGFFL
 24.9%; Score 718; DB 3; 34.0%; Pred. No. 4.1e-67; tive 96; Mismatches 229;
 547
 Length 556;
 Indels
 52;
 Gaps
 453
 222
 155
 517
 512
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 162
 117
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 397
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 ; MOLECULE TYPE: US-09-040-444-1
 Matches 194;
 Query Match
Best Local
 TELEFAX: (202)408-4400 INFORMATION FOR SEQ ID NO: 1:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION:
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 APPLICANT:
 394
398
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 223 TLITEFVGSGYR---RTTAILYQMAFTVGLVGLAGVAYAIPDWRWLQLAVSLPTFLFLLY
 216
 163
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 118
 STATE: D
 STREET: 1300 I S
CITY: Washington
 58
 STRANDEDNESS:
TOPOLOGY: lir
 96
 58
 TYPE:
 REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 24
 APPLICATION NUMBER: FILING DATE: March
 TELEPHONE:
 NAME: O'Connor, Steven
 Н
 1 MRDYDEVTAFLGEWGPFQRLIFFLL---SASIIPNGFTGLSSVFLIATPEHRCRVPDAAN 57
 LENGTH:
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 LLRTWNIRMYTIMSIMLWMTISVGYFGLSLDTPNLHGDIFVNCFLSAMVEVPAYVLAWLL
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 Similarity
 20005-3315
 amino acid
 D.C
 556 amino acids
 E: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P 1300 I Street, N.W., Suite 700
 USA
 Gorboulev, Valentin
 Conservative
 linear
 (202)408-4000
 March 18, 1998
 peptide
 single
 ----CEHGWVY--DTPGSSIVTEFNLVCGDAWKVDLFQSCVNLGFFL
 24.9%;
 Transport protein Which Effects The Transport Of Cationic Xenobiotics and\or Pharmaceuticals, DNA Sequences Encoding It And Their Use.
 US/09/040,444
 96; Mismatches 229; Indels
 Score 718; DB 3;
Pred. No. 4.1e-67;
 2481.1453-01
 #1.30
 Length 556;
 52;
 Gaps
 397
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 RESULT 5
US-08-501-572-2
 Sequence 2, Application US/08501572 Patent No. 6063623
 Query Match 24.8
Best Local Similarity 35.4
Matches 194; Conservative
 TELEFAX: (202)408-440 INFORMATION FOR SEQ ID NO:
 GENERAL INFORMATION:
 APPLICANT: Gorboulev
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
INVENTION:
NUMBER OF SEQUENCES:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 TELEPHONE: (202)408-4000
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Toohey Kimberlin M
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02481.1453-00000
 SEQUENCE CHARACTERISTICS:
 CORRESPONDENCE ADDRESS:
 APPLICANT:
 157
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 STREET: 1300 I S
CITY: Washington
 97
 58
 FILING DATE:
 88
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 COUNTRY:
 STATE:
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 amino acid
 20005-3315
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 553 amino acids
 Finnegan, Henderson, Farabow, Garrett & Dunner 1300 I Street, N.W., Suite 700
 (202)408-4400
(202)408-00: 2:
 Gorboulev, Valentin
 single)
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 Grundeman, Dirk
 USA
 Koepsell, Hermann
 peptide
 ----CQDGWVY--DTPGSSIVTEFNLVCADSWKLDLFQSCLNAGFFFG 162
 Transport protein Which Effects The Transport Of Cationic Xenobiotics and or Pharmaceuticals,
 DNA Sequences Encoding It And Their Use.
 24.8%; Score 714.5; DB 3; 35.4%; Pred. No. 9.6e-67; tive 87; Mismatches 216;
 US/08/501,572
 -----LATIA-NFSALG 96
 Length 553;
 Indels
 51;
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; MOLECULE TYPE: US-09-040-444-2
 RESULT 6
US-09-040-444-2
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 Sequence 2, Application Patent No. 6063766
 GENERAL INFORMATION:
 TELEFAX: (202)408-440 INFORMATION FOR SEQ ID NO:
 APPLICANT: GOIDOULEV
TITLE OF INVENTION:
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 ATTORNEY/AGENT INFORMATION:
NAME: O'CONNOY, Steven P
REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 24/
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 SEQUENCE CHARACTERISTICS:
 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 APPLICANT:
 APPLICANT:
 457
 398
 338
 335
 280
 517 GDALPETM 524
 514 GTPLPDTI 521
 275 WFIPESPRWLISOGRFEEAEVIIRKAAKANGIVVPSTIFDPSELQDLS$KKQQSHNILDL 334
 163 SLGVGYFADRFGRKLCLLGTVLVNAVSGVLMAFSPNYMSMLLFRLLQGLVSKGNWMAGYT
 TOPOLOGY:
 APPLICATION NUMBER: FILING DATE: March
 STRANDEDNESS:
 CLASSIFICATION
 COUNTRY:
 STREET:
 TELEPHONE:
 ADDRESSEE:
 LENGTH:
 QYLPRRYSMATALFLGGSVLLFMQLVPPDLYYLATVLVMVGKFGVTAAFSMVYVYTAELY 454
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 DRVGRIYPMAVSNLLAGAACLVI-FISPDLHWLNIIIMCVGRMGITTAIQMICLVNAELY
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 Washington
 amino acid
 20005-3315
 D.C
 E: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P. 1300 I Street, N.W., Suite 700
 553 amino acids
 Grundeman, Dirk
Gorboulev, Valentin
VENTION: Transport protein Which Effects Th
VENTION: Transport of Cationic Xenobiotics
 (202)408-4400
 USA
 Koepsell, Hermann
 (202)408-4000
 March 18, 1998
 single
 DNA Sequences Encoding It
 US/09040444
 US/09/040,444
 2
 2481.1453-01
 And Their
 The
 and\or Pharmaceuticals,
 Use.
 397
 337
 274
 456
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Local

Similarity

35.48;

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US-08-647-397-2
; Sequence 2, Application US/08647397
; Patent No. 5972702
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Matches
 GENERAL INFORMATION:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
CLASSIFICATION: 424
ATTORNBY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B00
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield &
 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 APPLICANT: Beier, David R. APPLICANT: Brady, Kevin P.
 SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
 457
 338
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 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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 STATE:
 STREET:
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 COUNTRY:
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 194; Conservative
 Boston
 MA
 600 Atlantic Avenue
 USA
 Floppy disk
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 σ
 US/08/647,397
 87;
 B0801/7048
 Pred. No. 9.6e-67;
7; Mismatches 216;
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 #1.25
 Indels
 51;
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 516
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 216
 162
 96
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 397
 337
 222
 156
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RESULT 8
US-08-964-127-2
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 Sequence 2, Application US/08964127
Patent No. 6277565
GENERAL INFORMATION:
 Matches
 Query Match
Best Local
 TELEPHONE: 617-720-2441
TELEPAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 2:
 APPLICANT: Grandearl, Andrew David John TITLE OF INVENTION: NOVEL GENES ENCODIN TITLE OF INVENTION: MOLECULES
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
 SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
 NUMBER OF SEQUENCES:
 518 KQEPEAEKASQTIPLKTG 535
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 398
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 279
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 219
 240
 161
 181
 103
 121
 ADDRESSEE: Fish a ... Street
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 61
 64
 COUNTRY:
 STATE:
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 VATFNGKKEEGEKLTVEELKFNLQKDITSAKVK-YGLSDLFRVSILRRVTFCLSLAWFAT
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 QDVYLSTIVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRKNVLFVTMGMQ 180
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 AFGYMVLPLFAYFIRDWRMLLVALTMPGVLCVALWWFIPESPRWLISQGRFEEAEVIIRK 299
 AASGSSAAFSPSLTVYMIFRFLCGCSISGISLSTIILNVEWVPTSTRAISSTTIGYC--Y
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 al Similarity
167; Conserv
02110-2804
 Boston
 MA
 Conservative
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 22.6%;
 545
 104; Mismatches
 Score 652.5; DB 2
Pred. No. 3.2e-60;
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 TRANSPORTER-LIKE
 DB 2;
 246;
 Indels
 Length 537;
 41;
 -QMLRV
 Gaps
 457
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 ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-964-127-2
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 Query Match
Best Local Similarity 22.5
 TELEX: 200154
INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
LENGTH: 520 amino acid
 NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567
REFERENCE/DOCKET NUMBER: 07334/038001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
TTORNING DATE:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FRASISEQ for Windows Version
 ATTORNEY/AGENT INFORMATION:
 281
 321
 266
 169
 117
 100
 541 MLKDGQ--ERPTILK 553
 159 ISGQLSDRFGRKNVLFVTMGM-------QTGFSFLQIFSKNFEMFVVLFVLVGM 205
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 40 VFLIATPEHRCRYPDAANLSSAWRNHTVPLRLRDGREVPHSCRRYRLATIANFSALGLEP 99
 TOPOLOGY:
 σ
 LSSKKQQSHNILDLLRTWNIRMVTIMSIM-LWMTISVGYFGLSLDTPNLHGDIFVNC--- 376
 GRDVDLGQLEQESCLDGWEFSQDVYLST-IVTEWNLVCEDDWKAPLTISLFFVGVLLGSF 158
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 10.5%; Score 302.5; DB 4; 22.5%; Pred. No. 2.7e-23; tive 98; Mismatches 231;
 2:
 2.0b
 Length
 Indels
 101;
 Gaps
 387
 64
 485
 20;
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 RESULT 9
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 US-09-496-692-2
 Best Local Similarity Matches 125; Conserva
 Sequence 2, Applic Patent No. 6313271
 Query Match
Best Local
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 520 amino acid
 GENERAL INFORMATION:
 ATTORNEY/AGENT INFORMATION:
NAME: Crews, Ph.D., L. L
REGISTRATION NUMBER: P-4
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/964,127
FILING DATE: 06-NOV-1997
 OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,692
 MOLECULE TYPE: FRAGMENT TYPE:
 TELECOMMUNICATION INFORMATION: 617/542-5070
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 CORRESPONDENCE ADDRESS
 APPLICANT:
 117 FLGYPADRFGRRGIVLLTLGLVGPCGVGGAAAGSSTGVMALR-----
 ADDITION OF THE TENT OF THE TE
 321 LSSKKQQSHNILDLLRTWNIRMVTIMSIM-LWMTISVGYFGLSLDTPNLHGDIFVNC---
 100 GRDVDLGQLEQESCLDGWEFSQDVYLST-IVTEWNLVCEDDWKAPLTISLFFVGVLLGSF 158
 65 P-----DFNHCLKDWDYNGLPVLTINAIGQWDLVCDLGWQVILEQLLFILGFASGYL 116
 40 VFLIATPEHRCRVPDAANLSSAWRNHTVPLRLRDGREVPHSCRRYRLATIANFSALGLEP 99
 TOPOLOGY:
 REGISTRATION NUMBER: P-43,567
REFERENCE/DOCKET NUMBER: 0733
 TELEX:
 TELEFAX:
 FILING
 COUNTRY:
 ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
 6 IFTLAPPLH-CHYGAFPPNASGWEQPPNASGVSVASAALAASAASRVATSTDPSCSGFAP
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 02110-2804
 amino acid
 DATE
 Application US/09496692
 200154
---ENTCPLPATSSFSFASLLNYRNIWKNL-----LILGFTNFIAHAIRHCYQP
 520 amino acids
 617/542-8906
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 Conservative
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 IBM Compatible
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 10.5%;
22.5%;
 MOLECULES
 Lee
 2:
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; Pred. No. 2.7e-23;
98; Mismatches 231;
 07334/038001
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 Indels 101;
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Gaps

20;

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376

280

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RESULT 10
US-09-031-392-5
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 ; MOLECULE TYPE: protein US-09-031-392-5
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 Sequence 5, Application US/09031392 Patent No. 5942398
 Matches
 Query Match
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
TYPE: amino acid
TOPOLOGY: linear
 ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
 APPLICANT: Tartaglia, APPLICANT: Weng, Xun TITLE OF INVENTION: N TITLE OF INVENTION: E
 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 TELEFAX: 01.
 448
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 144 LTISLFFYGYLLGSFISGQLSDRFGRK-----NVLFYTMGMQTGFSFLQIFSKNFEMFY 197
 486 VLRDGELCRRPSLLR 500
 541 MLKDGQ--ERPTILK 553
249 FAYFIRD-WRMLLVALIMPGVLCVALWWFIPESPRW-LISQGRFEEAEVIIRKAAKANGI 306
 COMPUTER: IBM COR
OPERATING SYSTEM:
 STREET: 225
CITY: Boston
 REFERENCE/DOCKET NUMBER: 35,
 APPLICATION NUMBER: US/09/031,392 FILING DATE: 26-FEB-1998
 Local Similarity
 MEDIUM TYPE:
 COUNTRY:
 ADDRESSEE:
 VYLGAYDRFLPYILMGSLTILTAILTLFLPESFGTPLPDTIDQMLRVKGMKHRKTPSHTR 540
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 02110-2804
 MA
 -----FLSAMVEVPAYVLAWLLLQYLPRRYSMATALFLGGSVLLFMQLVPPDLY- 425
 E: Fish & Richardson P.C.
225 Franklin Street
 USA
 617/542-8906
 Tartaglia, Louis A.
 Conservative
 IBM Compatible
 Diskette
 8.1%; Score 234; DB 2; Length 494
24.7%; Pred. No. 4.2e-16;
7ative 85; Mismatches 158; Indels
 NUCLEIC ACID MOLECULES ENCODING GLUTEX AND USES THEREOF
 Windows95
 07334/072001
 Length 494;
 98;
 Gaps
 485
 387
 177
 23;
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Вb
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 RESULT 11
US-09-299-549-5
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US-09-299-549-5
 Sequence 5, Application US/09299549 Patent No. 6136547 GENERAL INFORMATION:
 TELEX: 200154
INFORMATION FOR SEQ ID NO:
 OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
 APPLICATION NUMBER: 09/0 FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
 APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: GLUTEX AND USES THEREOF
 MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS
 PRIOR APPLICATION DATA:
 APPLICANT:
 NUMBER OF SEQUENCES:
 451 PETRGR----TFEEITRAFEGQVQTGTRGEKGP
 456
 336
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 TYPE: amino acid
TOPOLOGY: linear
 APPLICATION NUMBER: US/0 FILING DATE: 26-APR-1999
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 QGPRPAAMAVAGCSNWTSNFLVGLLFPSATFYLGAY----VFIVFTVFLVIFWVFTFFKV 450
 Meiklejohn, Ph.D.,
 02110-2804
 Boston
 ΜĀ
 494 amino acids
 225 Franklin Street
 USA
 Tartaglia, Louis A.
 IBM Compatible
 protein
 ---FKDAGVQEPVYATIGAGVVNTIFTVVSVFLVERAGRR--TLH 335
 10
 09/031,392
 US/09/299,549
 35,283
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 07334/072002
 Anita L.
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Query Match
Best Local Similarity

8.1%; Score 234; DB 4; 24.7%; Pred. No. 4.2e-16;

Length 494;

Matches

Conservative

85;

Mismatches

98;

Gaps

23;

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RESULT 12
US-09-610-417-5
 Sequence 5, Application US/09610417 Patent No. 6346374 GENERAL INFORMATION:
 TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
 451
 406
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 510 PESFGTPLPDTIDQMLRV-----KGMKHRKTP 536
 291
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 APPLICATION NUMBER: 09/299,549
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/0720
TELEPHONE: 617/542-5070
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,417
FILING DATE: 05-Jul-2000
 FILING DATE: 05-Ju PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GLUTEX AND USES THEREOF
 APPLICANT: Tartaglia, Louis A.
 LTISLFFVGVLLGSFISGQLSDRFGRK-----NVLFVTMGMQTGFSFLQIFSKNFEMFV
 QGPRPAAMAVAGCSNWTSNFLVGLLFPSATFYLGAY----VFIVFTVFLVIFWVFTFFKV 450
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 OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
 COMPUTER:
 ZIP: 02110-2804
 COUNTRY: USA
 STATE: MA
 CITY: Boston
LENGTH: 494 amino acids TYPE: amino acid
 TELEFAX: 617/542-8906
 -----FKDAGVQEPVYATIGAGVVNTIFTVVSVFLVERAGRR--TLH 335
 IBM Compatible
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ
US-09-610-417-5
 RESULT 13
US-08-964-127-4
 Sequence 4, Application US/08964127 Patent No. 6277565
 Best Local Similarity Matches 112; Conserv
 Query Match
Best Local
 GENERAL INFORMATION:
 OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/0 FILING DATE: 06-NOV-1997 PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
 NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
 APPLICANT: Grandearl, Andrew David John
TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER LIKE
TITLE OF INVENTION: MOLECULES
 ATTORNEY/AGENT INFORMATION:
 ADUNE
STREET: 2-
STREET: 4A
 451 PETRGR----TFEEITRAFEGQVQTGTRGEKGP 479
 336
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 FILING DATE:
 COMPUTER:
 COUNTRY: USA
ZIP: 02110-2804
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 REGISTRATION
 APPLICATION NUMBER:
 NAME:
 FAYFIRD-WRMLLVALTMPGVLCVALWWFIPESPRW-LISQGRFEEAEVIIRKAAKANGI 306
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 AQ-----DIQEMKDESMRMSQEKQVTVLELFRAPNYRQPIIISIMLQLSQQLSGINAVFY
 Crews,
 225 Franklin Street
 IBM Compatible
 Conservative
, Ph.D., L. Lee
NUMBER: P-43,567
 8.1%;
 US/08/964,127
 85;
 Score 234; DB 4;
Pred. No. 4.2e-16;
 ID NO:
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 Version 2.0b
 ----VLAWLLLQYLPRRYSMAT 405
 158;
 Length
 Indels
 98;
 Gaps
 394
 335
 290
 177
 248
 23;
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REFERENCE/DOCKET NUMBER:

07334/038001

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 US-09-496-692-4
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 US-08-964-127-4
 Sequence 4, Application US/09496692 Patent No. 6313271
 Matches
 Query Match
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
 OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
 TITLE OF INVENTION:
 FRAGMENT TYPE:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
ATTORNEY/AGENT INFORMATION:
NAME: CIEWS, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567
REFERENCE/DOCKET NUMBER: 07334/038001
TELECOMMUNICATION INFORMATION:
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 TELEFAX: 61.,
TELEFAX: 200154
 PRIOR APPLICATION DATA:
 TYPE: ami
TOPOLOGY:
 266 PGVLCVALWW--FIPESPRWLISQGRFEEAEVIIRKAAKAN 304
 169 D-----LGVYLMRLELCDPTQRLRVALAGELVGVGGHFLFLGL-ALVSKDWRFLQRMITA 222
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CITY: E
 65 P-----DFNHCLKDWDYNGLPVLTTNAIGQWDLVCDLGWQVILEQILFILGFASGYL
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 COUNTRY: USA
ZIP: 02110-2804
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 APPLICATION NUMBER: FILING DATE:
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 6 IFTLAPPLH-CHYGAFPPNASGWEQPPNASGVSVASAALAASAASRVATSTDPSCSGFAP
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 Boston
 MA
 3: Fish & Richardson P.C. 225 Franklin Street
 617/542-8906
 Grandearl,
 Conservative
 linear
 IBM Compatible
 protein
internal
 MOLECULES
 7.4%; Score 214.5; DB 4;
24.6%; Pred. No. 2.1e-14;
tive 51; Mismatches 122;
 1, Andrew David John NOVEL GENES ENCODING TRANSPORTER-LIKE
 US/09/496,692
 4:
 2.0b
 Length
 286;
 39;
 168
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 US-09-496-692-4
 US-08-355-844-3
 Query Match
Best Local S
Matches 69
 Sequence 3, Application US/08355844 Patent No. 5940307
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355
FILING DATE: 14-DEC-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Tang, Henry Y.S.
REGISTRATION NUMBER: 29,705
REFERENCE/DOCKET NUMBER: A299
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 286 amino acid
 TOPOLOGY: 11:
MOLECULE TYPE:
FRAGMENT TYPE:
 APPLICANT: Cheung, M: TITLE OF INVENTION: 7
TITLE OF INVENTION: 7
NUMBER OF SEQUENCES:
TELECOMMUNICATION INFORMATION: TELEPHONE: 212-408-2586
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 CORRESPONDENCE ADDRESS:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 117 FLGYPADRFGRRGIVLLTLGLYGPCGYGGAAAGSSTGYMALR-----FLLGFLLAGV 168
 266 PGVLCVALWW--FIPESPRWLISQGRFEEAEVIIRKAAKAN 304
 100 GRDVDLGQLEQESCLDGWEFSQDVYLST-IVTEWNLVCEDDWKAPLTISLFFVGVLLGSF 158
 206 GQISNYVAAFVLGTEILGKSVRIIFSTLGVCIFYAFGYMVLPLFAYFIRDWRMLLVALTM 265
 159 ISGQLSDRFGRKNVLFVTMGM------QTGFSFLQIFSKNFEMFVVLFVLVGM 205
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
 STREET: 30 Roc
CITY: New York
 65 P------DENHCLKDWDYNGLPVLTTNAIGQWDLVCDLGWQVILEQILFILGFASGYL 116
 40 VFLIATPEHRCRVPDAANLSSAWRNHTVPLRLRDGREVPHSCRRYRLATIANFSALGLEP 99
 TYPE:
 TELEFAX:
 ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond STREET: 30 Rockefeller Plaza
 COUNTRY:
 6 IFTLAPPLH-CHYGAFPPNASGWEQPPNASGVSVASAALAASAASRVATSTDPSCSGFAP 64
 PCILFLEYGWPGLFLESARWLIVKRQIEEAQSVLRILAERN 263
 D-----LGVYLMRLELCDPTQRLRVALAGELVGVGGHFLFLGL-ALVSKDWRFLQRMITA
 l Similarity
69; Conserv
 RY: USA
10112-0228
 amino acid
 20015
 ΥN
 286 amino acids
 Cheung, Min
 Czegledy, Ferenc
 Conservative
 617/542-8906
 PatentIn Release #1.0, Version #1.25
 Iserovich, Pavel
 Fischbarg, Jorge
 linear
 internal
 protein
 24.6%;
 STRUCTURE
 A METHOD FOR PREDICTING PROTEIN
 7.4%; Score 214.5; Ds 4;
24.6%; Pred. No. 2.1e-14;
 US/08/355,844
 4:
 A29927-50/29910
 Length
 Indels
 286;
 39;
 Gaps
```

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TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Human
FEATURE:
NAME/KEY: Peptide
LOCATION: 1.492
OTHER INFORMATION: Fac:
OTHER INFORMATION: Glut
US-08-355-844-3
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Search completed: July 17, 2002, 02:03:58 Job time: 5774 sec
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 INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 Ouery Match 7.2%; Score 208; DB 2; Length 492; Best Local Similarity 22.2%; Pred. No. 2.3e-13; Matches 108; Conservative 87; Mismatches 165; Indels 126; Gaps
 474 QSDKTP 479
 531 KHRKTP 536
 362 PWMSYLSIVAI----FGFVAFFEVGPGPIPWFIVAELESQGPRPAAIAVAGFSNWTSNFI 417
 422
 302 GVQQPVYATIGSGIVNTAFTVVSLFVVERAGRRTLHLIGLAGMAGQAILMTIALALLEQL 361
 255
 330 ---NILDLLRTWNIRMYTIMSIMLWMT-----ISVGYFGLSLDTPNLHGDIFVNCFLSA 380
 206
 276 FIPESPRW-LISQGRFEEAEVIIRKAAKANGIVVPSTIFDPSELQDLSSKKQQSH----- 329
 157 GTLHQLGIVVGILIAQVFGL-------DSIMGNKDLWPLLLSIIFIPALLQCIVIP 205
 231
 119 FSQDYYLSTIVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRK------NV 172 : : : : : | | : : | | : : : | | : : | | : : | | : : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 52 YGESILPTTLTTLWS-----LSVAIFSVGGMIGSFSVGLFVNRFGRRNSMLMMNL 101
 PDLYYLATVLVMVGKFGVTAAFS-----MVYVYTAELYPTVVRNMGVGVSSTASRLGS-I 475
 KKVTILELFRSPAYRQPILIAVVLQLSQQLSGINAVFYYSTSI-----FEKA 301
 FCPESPRFLLINRNEENRAKSVLKKLRGTADVT------HDLQEMKEESRQMMRE 254
 LSPYFVYL----GAYDRFLPYILMGSLTILTAILTLF-LPESFGTPLPDTIDQMLRVKGM 530
 STL------GVCIFYAFGYMVLPLFAYFIRD------WRMLLVALTMPGVLCVALWW 275
 Facilitative glucose transportor Glut1 protein
 ω
 22;
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Title:
Perfect score:
Sequence:
 Result
No.
 Total number of hits satisfying chosen parameters:
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB
Maximum DB
 Scoring table:
 Run on:
 OM protein - protein search, using sw model
 Database
 Searched:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
 seq
 length: 0
length: 2000000000
 PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
 Query
Match
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2883
1 MRDYDEVTAFLGEWGPFQRL.....HTRMLKDGQERPTILKSTAF 557
 July 17, 2002, 02:05:09; Search time 58.69 Seconds (without alignments)
 283138 seqs, 96089334 residues
 Gapop 10.0 ,
 BLOSUM62
 GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
 Length DB
 Gapext 0.5
C88485
T25829
H86298
C88504
T23190
AC3602
AR3602
AR32854
AR32854
AR32854
AR32854
AR360300
AR32854
AR360300
AR360300
AR360300
AR360300
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 JW0089
JE0346
T220346
T2203484
S50862
T27870
T16565
T01019
D89646
C96758
B86299
T21682
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hypothetical prote
transport protein
protein ZK455.8 [i
probabile protein
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| OV                                                                 | Db<br>Db                                                         | Qy<br>Qy<br>Db                                               | B 6 B 6                                                            |                                                                                 | Me<br>Me                                   | RESULT<br>JW008<br>Organ<br>N;Alt<br>C;Acc<br>C;Acc<br>C;Acc<br>C;Acc<br>Rioch<br>Bioch<br>Bioch<br>Bioch<br>A;Tit<br>A;Tit<br>A;Res<br>A;Res<br>A;Res<br>A;Res<br>A;Exp                                 |            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|--------------------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------------|---------------------------------------------------------------------------------|--------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 421                                                                | 361<br>361                                                       | 241<br>241<br>301<br>301                                     | 121<br>121<br>181<br>181                                           | , 6 6 L L                                                                       | Query Ma<br>Best Loo<br>Matches            | RESULT 1 JW0089 organic cati N;Alternate C;Speciles: H C;Date: 18-J C;Accession: R;Wu, X.; pri Biochem. Bio A;Title: cDN A;Reference A;Accession: A;Molecule t A;Rcoss-refe A;Experiment: T C;Comment: T |            | 330<br>331<br>332<br>333<br>333<br>335<br>335<br>336<br>337<br>337<br>337<br>337<br>337<br>337<br>337<br>337                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|                                                                    |                                                                  |                                                              |                                                                    | MRDYDEV MRDYDEV AWRNHTV                             AWRNHTV                     |                                            | on trans names: ( como sapi un-1998 JW0089 asad, p. phys. Re A sequer number: JW0089 ype: mRY 1-557  1-557  1-557                                                                                        |            | 295.5 10.2<br>291.5 10.1<br>287 10.0<br>279 9.7<br>277 9.5<br>277 9.4<br>277 9.4<br>277 9.4<br>277 9.4<br>267 9.3<br>267 9.3<br>267 9.3<br>267 9.3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| VMVGKEGVTAAF                                                       | IFVNCFLSAMVE                                                     | FIRDWRMLLVAI                                                 | WINT CELLWAKAE                                                     | GEWGPFQRLIFE<br>GEWGPFQRLIFE<br>GEWGPFQRLIFE<br>RDGREVPHSCRE<br>                | 100.0%;<br>ty 100.0%;<br>ervative          | KT DE CO O ST                                                                                                                                                                                            |            | 44444444444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| SMVVVVTAFI                                                         | EVPAYVLAWLL<br>         <br> VPAYVLAWLL                          | JTMPGVLCVAL                                                  | TITISLEFYGY THISLEFYGY THISLEFYGY THISLEFYGY THISLEFYGY THISLEFYGY | TLSASIIPNG TLSASIIPNG TLSASIIPNG RYRLATIANFS RYRLATIANFS RYRLATIANFS            | Score 2883;<br>Pred. No. 1<br>0; Mismatche | ision ision f.H.; 6, 589 funct 982895                                                                                                                                                                    | ALIGNMENTS | \$74046<br>T15290<br>C69757<br>G72234<br>T27082<br>B90498<br>S39461<br>T33985<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T23608<br>T2 |
| PPDLYYLATVLVMVGKFGVTAAFSMVYVYDA.TFATVPTVVTANAGVGVSSTASRI.GSTI.SPYF | LSLDTPNLHGDIFVNCFLSAMVEVPAYVLAWILLQYLPRRYSMATALFLGGSVLLFMQLV<br> | FGYMVLPLFAYFIRDWRMLLVALTMPGVLCVALWWFIPESPRWLISQGRFEEAEVIIRKA |                                                                    | MRUYLDEVTARIGEWGFFQKLIFFLLSASIIPNGFTGLSSYFLATPEHKCKYPDAANLSS                    | . 1.7e-212;<br>ches 0; In                  | 1998 #text<br>hy, v.<br>998<br>d genomic<br>d genomic                                                                                                                                                    | NTS        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| TASRIGSTISPYF                                                      | FLGGSVLLFMQLV                                                    | GRFEEAEVIIRKA                                                | GRKNVLFVIMGMQ GRKNVLFVIMGMQ GRKNVLFVIMGMQ IIFSTLGVCIFYA            | HRCRYDAANLSS HRCRYDAANLSS HRCRYDAANLSS LEQESCLDGWEFS LINE HILLING LEQESCLDGWEFS | Length 557;<br>Indels 0; Ga                | nge 28-M<br>nization                                                                                                                                                                                     |            | probable sugar hypothetical p transporter ho hypothetical p hypothetical p hypothetical p permease, prob synaptic vesic hypothetical p hypothetical p hypothetical p hypothetical p probable trans                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 480                                                                | 420<br>420                                                       | 300<br>300<br>360<br>360                                     | 180 240 240                                                        | 60<br>60<br>120<br>120                                                          | aps 0;                                     | lay-1999  of human OCTN2, g3273741  drugs and other                                                                                                                                                      |            | sugar tra ical prote ical prote ical prote ical prote ical prote ical prote probable vesicle p ical prote transport transport                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |

Qy

421 PPDLYYLATVLVMVGKFGVTAAFSMVYVYTAELYPTVVRNMGVGVSSTASRLGSILSPYF 480

319/3;

358/2;

490/3;

Gaps

6,

61

75

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JEG346
high-affinity carntine transporter, CT1 - rat
C:ppecies: Rattus norvegicus (Norway rat)
C:pate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Ju
C:pate: No. Secsion: JE0346
A:Fitle: Molecular cloning and characterization of high-affinity carn
A:Reference number: JE0346
A:Status: preliminary
A:Molecule type: manNA
A:Residues: 1-57 <SEK>
A:Cross-references: DDBJ:AB017260; NID:g3869208; PIDN:BAA34399.1; PID
A:Cross-references: DDBJ:AB017260; NID:g3869208; PIDN:BAA34399.1; PID
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Matches 475
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 421
 181
 121
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 61
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Pred. No. 6.2e
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 16-Jul-1999 #text_change 21-Jul-2000
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 Indels
 Sugiyama, Y.; Kanai,
 0;
 PID:g3869209
 Gaps
 540
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C;Accession: JC4884
R;Okuda, M.; Saito, H.; Urakami, Y.; Takano, M.;
Biochem. Biophys. Res. Commun. 224, 500-507, 199
A;Title: cDNA cloning and functional expression
A;Reference number: JC4884; MUID:96295517
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1996 #sequence_revision 18-Oct-1996 #text_change
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 A; Gene: CESP:F521
A; Map position: (
A; Introns: 16/1;
 A; Reference number: Z19573
A; Accession: T22509
A; Status: preliminary; translated
 submitted to the EMBL Data A; Reference number: 219573
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 A;Experimental source: clone
C;Genetics:
 JC4884
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 A; Molecule type: DNA
A; Residues: 1-576 <WIL>
 A; Cross-references: EMBL: Z83228; PIDN: CAB05732.1;
 Query
Best L
 Genetics:
 Matches
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 477
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 364
 357
 304
 302
 244
 185
 125
 182
 122
 Y Match
 76
 62
 16
 ω
 CESP: F52F12.1
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 DVYLSTIVTEWNLVCEDDWKAPLTISLFFYGYLLGSFISGQLSDRFGRKNYLFYTMGMQT 181
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 al Similarity
165; Conserv
 23/3;
 Conservative 118;
 50/1;
 27.0%;
 Library,
 80/3;
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 Score 777;
Pred. No. 1
 from
 108/2; 134/3; 221/1;
 December
 Mismatches
 GB/EMBL/DDBJ
 15-Oct-1999 #text_change 15-Oct-1999
 3
 DB 2; I
1.3e-51;
hes 225;
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 Inui,
 GSPDB:GN00019; CESP:F52F12.1
 Length
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 Indels
 257/2;
 522
 rat kidney organic
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05-Nov-1999

cation

416

363

356 303 301 241 184

243

423

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A;Molecule type: mRNA
A;Residues: 1-556 <GRU>
A;Cross-references: EMBL:X78855;
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Nov-1999
C;Accession: S50862; S78533; I58089
 RESULT
S50862
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 Db
 Qy
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 Qy
 Qy
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 Qy
 C; Comment: This protein is responsible for the transport of cationic
 A;Accession: JC4884
A;Molecule type: mRNA
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A;Cross-references: DDBJ:DB3044; NID:91502282;
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A; Accession: S78533
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 A; Experimental source: kidney R; Gorboulev, V.G.
 A;Title: Drug excretion mediated by a new A;Reference number: I58089; MUID:95082907 A;Accession: S50862
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 submitted to the EMBL Data Library,
 R; Gruendemann,
 VΩ
 Nature 372, 549-552, 1994
 Query Match
Best Local S
Matches 198
 520
 465
 461
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 405
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 231
 224
 171
 164
 113
 104
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 59
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 TID----
 TIEDAENMQRPRKKERKENLPPS
 MGVGVSSTASRLGSILSPYFVY-LGAYDRFLPYILMGSLTILTAILTLFLPESFGTPLPD 519
 SDRFGRKNVLFVTMGMQTGFSFLQIFSKNFEMFVVLFVLVGMGQISNYVAAFVLGTEILG
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 MYTIMSIMLWMTISVGYFGLSLDTPNLHGD-IFVNCFLSAMVEVPAYVLAWLLLQYLPRR
 KSVRIIFSTLGVCIFYAF--GYMVLPLFAYFIRDWRMLLVALTMPGVLCVALWWFIPESP
 ADRFGRKFCLLVTILINAISGALMAISPNYAWMLVFRFLQGLVSKAGWLIGYILITEFVG
 DRNQLPLGPCEHGWYYNTPG--SSIVTEFNLVCAHSWMLDLFQSVVNVGFFIGAMMIGYL
 SQRCGWSQAEELNYTVPGLGPSDEASFLSQCMRYEVDWNQSTLDCVDPLSSLA-----A
 RWLISQNKIVKAMKIIKHIAKKNGKSVPVSLQNLTPDEDAGKKLKPS--ILDLVRTPQIR
 RWLISQGRFEEAEVIIRKAAKANGIVVPSTIFDPSELQDLSSKKQQSHNILDLLRTWNIR
 LGYR----RMVGICYQIAFTVGLLILAGVAYVIPNWRWLQFAVTLPNFCFLLYFWCIPESP
 SS--AWR-----NHTVP-LRLRDGREVPHSCRRYR------LATIANFSALGLEPGRDV 103
 MSTVDDILEHIGEFHLFQKQTFFLL--ALLSGAFTPIYVGIVFLGFTPDHHCWSPGAAKL
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 25.4%;
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 Score 733; DB 2;
Pred. No. 3.1e-48;
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 PIDN:CAA55411.1;
 PIDN:BAA11754.1; PID:d1012421;
 Veyhl,
 234;
 Length 593;
 Indels
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 Koepsell,
 PID: g633622
 Gaps
 drugs in
 524
 464
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 58
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 kidney.
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Caenorhabditis elegans

15-Oct-1999

#text\_change

18-Feb-2000

RESULT T27870

A; Reference number: Z20432

Library,

November

1995

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A;Residues: 1-342,'N',344-556 <GOR>
A;Cross-references: EMBL:X78855; NID:g633621; PIDN:CAA55411.1; C;Keywords: glycoprotein; phosphoprotein; transmembrane protein F;20-46/Domain: transmembrane #status predicted <TM1> F;178-197/Domain: transmembrane #status predicted <TM2> F;178-197/Domain: transmembrane #status predicted <TM3> F;243-260/Domain: transmembrane #status predicted <TM3>
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 Qy
 Q
 Qy
 Qy
 Ωy
 Qy
 F;71,97,113,432/Binding site: carbohydrate (Asn) (covalent) #status predicted F;286,292/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status F;296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #sta
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F;469-485/Domain: transmembrane #status predicted <TM10>
F;494-514/Domain: transmembrane #status predicted <TM11>
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 F; 267-283/Domain: F; 350-366/Domain:
 Best Local Similarity Matches 193; Conserv
 Query Match
Best Local :
518 KGVALPETIEEAENL-GRRKSKAKENTIYLQ
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 454
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 394
 338
 334
 223
 216
 163
 156
 118 PLGP----
 96
 58
 58
 ш
 1 MRDYDEVTAFLGEWGPFQRLIFFLL---SASIIPNGFTGLSSVFLIATPEHRCRVPDAAN
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 WWFIPESPRWLISQGRFEEAEVIIRKAAKANGIVVPSTIFDPSELQDLSSKKQQSHNILD
 TLITEFVGSGYR----RTTAILYQMAFTVGLVGLAGVAYAIPDWRWLQLAVSLPTFLFLLY 279
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 LSS--AWR-----NHTVP-LRLRDGREVPHSCRRYRL-----
 LFRTPTLRKHTVILMYLWFSCAVLYQGLIMHVGATGANLYLDFFYSSLVEFPAAFIILVT
 LSQRCGWSQAEELNYTVPGLGPSDEASFLSQCMRYEVDWNQSTLDCVDPLSSLVANRSQL
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 #status
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pred

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T16565
hypothetical protein K05F1.6 - Caenorhabditis el C; Spectles: Caenorhabditis elegans
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-19
C; Accession: T16565
R; Wohldmann, P.
submitted to the EMBL Data Library, June 1995
A; Description: The sequence of C. elegans cosmic A; Reference number: Z18537
A; Accession: T16565
A; Status: preliminary; translated from GB/EMBL/I
 A; Accession: T27870
A; Status: preliminary; translated fr.
A; Molecule type: DNA
A; Residues: 1-794 <WIL>
A; Cross-references: EMBL: 266567; PID
A; Cross-references: conce ZK455
C; Genetics: A; Gene: CESP: ZK455.8
A; Map position: X
A; Introns: 52/3; 119/2; 158/1; 207/3
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 Matches 167;
 Query Match
Best Local
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 155
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 Local Similarity
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 SPRWLISQGRFEEAEVIIRKAAKANGIVVPSTIFDPSELQDLSSKKQQSHN----ILDLL
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 20-Sep-1999
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 388
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A; Molecule type: DNA
A; Residues: 1-745 <WOH>
A; Cross-references: EMBL:U29377; NID:g868173;
A; Experimental source: strain Bristol N2
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A; Experimental source: cultivar Columbia
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 A; Status: translated from GB/EMBL/DDBJ
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 CESP: K05F1.6
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 TPN----LHGDIFVNCFLSAMVEVPAYVLAWLLLQYLPRRYSMATALFLGGSVLLFMQLVP
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 546/2;
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 ATSP:YU
 680/3
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A; Map position:

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protein ZK455.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C:Accession: D89646
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; pMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D89646
A:Status: preliminary
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A:Residues: 1-447 <STO>
A:Cross-references: GB:chr_X; PIDN:CAA91492.1; PID:g3881642; GSPDB:GN00028; CESP:ZK455.8
A:Note: Similarity to sugar transporters
C:Gene: ZK455.8
A:Map position: X
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 Matches
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 504
 444
 386
 403
 273
 299
 156
 184
 125
 98
 89
 65
 22
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 LPDTIDQ 523
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maîti, I Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, A;Authors: Sulzberg, S.L.; Schwartz, J.R.; Shinn, D.; Davis, R.W.

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
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 probablle protein transporter T18K17.11 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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 A; Status: preliminary
 A; Accession: C96758
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 Query Match
Best Local S
Matches 157
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hypothetical protein F309.19 - Arabidopsis thaliana
() Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, F.
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kraul, S.; White, O.; Alons
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, F.
Anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E., Kim, A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Maiti, R.; Marzial
A; Anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Maiti, R.; Marzial
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
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A; Status: preliminary
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 Query Match
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 522
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 523 AQ 524
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 hypothetical protein F32H5.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t/C;Accession: T21882 R;Steward, C.
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 A;Cross-references: EMBL: Z81524; PIDN: CAB04250.1; A; Experimental source: clone F32H5
 A; Molecule type: DNA
A; Residues: 1-528 <WIL>
 A; Gene: CESP:F32H5.4
 A; Status: preliminary; translated
 A; Accession: T21682
 A; Reference number: Z19458
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 317 ELQDLSSKKQQSHNILDLLRTWNIRMYTIMSIMLWM---TISVGYFGLSLDTPNLHGDIF 373
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 206
 263
 520
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 264
 282
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 18;
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R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biologa; Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el.
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an A;Accession: C88485
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C88485
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A; Residues: 1-751 <STO>
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 QY
 A; Status: preliminary
hypothetical protein T01B11.5 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *te
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Matches 106
 position:
 434
 456
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 127 TIVTEWNLVC-EDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRKNVLFVTMGMQTGFSF
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C; Accession; Geisel,
 R;Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid T01B11.
A;Reference number: Z20099
A;Accession: T25851
A;Status: preliminary; translated from GB/EMBL/DDBJ
C;Accession: B96825
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: B96825
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A; Introns: 85/1
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 A; Experimental source: strain C; Genetics:
 A;Cross-references: EMBL:U80931; PIDN:AAB38002.1; GSPDB:GN00022; A;Experimental source: strain Bristol N2; clone T01B11
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 C.J.; Federspiel, N.A.; Kaul, S.; White, Conway, A.B.; Conway, A.R.; Creasy, T.H.;
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 Gaps
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 132
 269 LCVALWWFIPESPRWLISQGRFEEAEVIIRKAAKANGIVVPSTIFDPSELQDLSSKKQ-Q 327 ::::| | | | | | | : : : |
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 156 GSFISGOLSD-RFGRKNVLFVT---MGMQTGFSFLQIFSKNFEMFVVLFVLVGMGQISNY 211
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Maximum Match 100%
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 Sequence:
 Title:
Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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saccharomyc
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R klebsiella
4 kluyveromyc
0 escherichia
2 canis famil
4 bacillus su
3 bacillus su
9 homo sapien
3 ovis aries
bos taurus
escherichia
 rattus norv
bos taurus
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| R                   | RA<br>RA                                                       | R 및                     | R P         | RRT          | RA                      | RA                 | R R        | Z 2         | <sup>꼭</sup> ~        | RA                 | RA                                    | R R R               | RE        | R R                    | RA R                | R 70 7      | RR  | R R                 | RT RA                            | RP                                             | XOX        | 888                          | GN         | DE                    | DJ DJ                |           | 2 U S                    | RES      |            |                                          |             |             |                            |         |                    |  |
|---------------------|----------------------------------------------------------------|-------------------------|-------------|--------------|-------------------------|--------------------|------------|-------------|-----------------------|--------------------|---------------------------------------|---------------------|-----------|------------------------|---------------------|-------------|-----|---------------------|----------------------------------|------------------------------------------------|------------|------------------------------|------------|-----------------------|----------------------|-----------|--------------------------|----------|------------|------------------------------------------|-------------|-------------|----------------------------|---------|--------------------|--|
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| arnitine t          | Burwinkel B., Kreuder J., Schweitz Gerbitz KD., Kilimann M.W.; | RIANT CDSF              | Pharmacol   | tion trans   | en J., Con<br>unctional | X., Huang          | ARACTERIZA | Nat. Genet. | "Primary syst         | shino M.,          | Nezu J., Tam<br>Nikaido H.,           | SEQUENCE FROM N     | Biol. Che | olecular a             | nai I., Oh          | SSUE=Kidney |     | OCTN2, a new        | X., Prasad P<br>DNA sequence,    | SEQUENCE FROM N.A. MEDLINE=98289574; PubMed=96 | BI_TaxID=9 | mmalia: Eu                   | C22A5 OR C | mber 5) (E            | -OCT-2001            | -OCT-2001 | MAN<br>N2_HUMAN<br>6082: | <b>-</b> |            | 206.5                                    |             |             | 213.5                      | 217     | 219<br>21 <b>7</b> |  |
| ranspo              | , Kreu                                                         | GLN-1                   | Exp.        | porter<br>". | way S.                  | W., P              | TION.      |             | temic                 | Kato H.,           | Υ.Ή                                   | ٠ <del>.</del><br>۲ | m. 273:   | nd func                | . <u>.</u> .        | 7 .         | , , | e a                 | id P.D.<br>ice, tr               | M N.A.                                         | 606;       | (nulla<br>Metazoa<br>Metazoa | CTN2.      | .on/car<br>ligh-af    | (Rel.                | (Rel.     | STA                      |          |            | 7.2                                      |             |             |                            |         |                    |  |
| rter o              | der J.,<br>imann N                                             | 69.<br>Pub <b>m</b> ed= | Ther.       | 2 (00)       | J., Gan<br>terist:      | rasad F            |            | 94 (1999    | temic carnitin        | ., Ohur            | Oku A., (                             | PubMed=             |           | ctional<br>nitine      | ., Nezu             | Dish Madi   |     | r of t              | .D., Leiba                       | PubMed:                                        |            | ; Chordat<br>; Primate       |            | nitine<br>finity      | 40, Las              | 40, cr    | NDARD;                   |          |            | 567<br>547                               | 91          | -4-         | 800                        | 999     | 9 9                |  |
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| mutati              | hweitze<br>;                                                   | 25211:                  | :1482-1     | , an or      | thy V.;<br>and tis      | 54528;<br>, Seth   | 1          |             | efic                  | 5                  | hi F                                  | 6797:               | - 12      |                        | -I., Ya             | 300         |     | er of the organic c | F.H., (                          | 8255;                                          |            | ; Craniata;                  | ,          | nsporte<br>ium-dep    | nnotati              | d)        | PRT;                     |          | ALIC       | HXTA_YEAST<br>GTR1_LEIDO                 | GTR3_R      | PCAK_PS     | GTR1_R                     | GTR3_CF | GTR3_M             |  |
| ions in systemic pr | er S., Vorgerd M., G                                           |                         | 1492(1999). | ganic c      | sue distribution p      | P., Rajan D.P., Le |            |             | tiency is caused by m | imoto G., Hayakawa | ., Yabuuchi H., Ha<br>ii Y., Takada G |                     |           | fication of sodium ion | abuuchi H., Oku A., |             | Ç   | ation transporte    | napathy V.;<br>and genomic organ |                                                |            | Vertebrata;                  |            | carrie<br>tine c      | ist sequence update) |           | 557 AA.                  |          | ALIGNMENTS | EAST<br>EAST<br>EIDO                     | AT          | SEPU        | ABIT                       | HICK    | OUSE               |  |
| imary c             | empel                                                          |                         |             | ine          | ttern                   | ibach F            |            |             | mutation              | Sh                 | 210                                   |                     |           | n-dependent,           | Shiman              |             |     | c family.           | ization                          |                                                |            | Euteleostomi                 |            | er family<br>otranspo |                      |           |                          |          |            | P40885<br>P54862<br>Q01440               | 007647      | Q51955      | P13355                     | P28568  | P32037             |  |
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 MEDLINE=20145665; PubMed=10679939; Wang Y., Kelly M.A., Cowan T.M., Longo "A missense mutation in the OCTN2 gene carnitine transport activity."; Hum. Mutat. 15:238-245(2000).
 "Two novel missense mutations of the OCTN2 gene (W283R patient with primary systemic carnitine deficiency."; Hum. Mutat. 15:118-118(2000).
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 "Mutations in novel organic cation transporter (OCTN2), an organic cation/carnitine transporter, with differential effects on the organic cation transport function and the carnitine transport
 Seth
 Hum.
 Tang N.L., Ganapathy V., Wu X., Hui J., Seth P., Yuen P.M., Wanders R.J., Fok T.F., Hjelm N.M.; "Mutations of OCTN2, an organic cation/carnitine transporter, lead to deficient cellular carnitine uptake in primary carnitine deficiency Hum. Mol. Genet. 8:655-660(1999).
 "Identification of two novel mutations systemic carnitine deficiency."; Hum. Genet. 105:157-161(1999).
 VARIANTS CDSP ARG-283 AND PHE-446.
MEDLINE-20081068; PubMed-10612840;
 MEDLINE=20026865;
 VARIANT
 Vaz F.M., Scholte H.R., Ruiter J., Rodrigues Pereira R., Schweitzer S
 MEDLINE-99408248;
 Mayatepek E.,
 CHARACTERIZATION OF VARIANT CDSP LEU-478,
 MEDLINE-99172075;
 VARIANT CDSP CYS-211.
 VARIANT CDSP LYS-452
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 MYOPATHY OR CARDIOMYOPATHY SIMILARITY: BELONGS TO THE CATION SUBFAMILY.
 SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY, SKELETAL MUSCLE,
 CARNITINE DEFICIENCY (CDSP). CDSP IS AN AUTOSOMAL RECESSIVE DISONDER OF FATTY ACID OXIDATION CAUSED BY DEFECTIVE CARNITINE TRANSPORT. PRESENT EARLY IN LIFE WITH HYPOKETOTIC HYPOGLYCEMIA ACUTE METABOLIC DECOMPENSATION, OR LATER IN LIFE WITH SKELETAL
 HEART AND PLACENTA.
DISEASE: DEFECTS IN SLC22A5 ARE THE CAUSE OF SYSTEMIC PRIMARY
 FUNCTION: SODIUM-ION DEPENDENT, HIGH AFFINITY CARNITINE TRANSPORTER. ALSO TRANSPORTS ORGANIC CATIONS WITHOUT THINVOLVEMENT OF SODIUM. INVOLVED IN THE ACTIVE CELLULAR I
 ; AF057164; AAC24828.1;
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; AB016625; BAA36712.1;
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Huang W., Leibach F.H.,
 PubMed=10072434;
 PubMed-10480371;
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 J.,
 with an unconventional splicing abnormality."; es. Commun. 261:484-487(1999).
 Tamai I.,
 SUGAR TRANSPORTER FAMILY. ORGANIC
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 Oku A., Katsura M.,
 Hussaarts-Odijk L.M., , de Klerk J.B.C., Wa
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Transmembrane; Glycoprotein;
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M > R: LOSS OF BOTH CARNIFINE AND CATION TRANSPORT FUNCTIONALITIES.

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E -> K (IN CDSP)
 /FTId=VAR_009252.
Y -> C (IN CDSP)
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 Disease mutation
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 (POTENTIAL).
 CARNITINE ORGANIC CATION
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 J. Pharmacol. Exp. Ther. 290:1482-1492(1999).

-I. FUNCTION: SODIUM-ION DEPENDENT, HIGH AFFINITY CARTONS WITH TRANSPORTER, ALSO TRANSPORTS ORGANIC CARTONS WITH INVOLVEMENT OF SODIUM. INVOLVED IN THE ACTIVE CELOCATIONE.

-I. SUBCELLULAR LOCATION: Integral membrane protein.
-I. SUBCELLULAR LOCATION: INTEGRAL THE CAUSE OF JUV.

STEATOSIS (JVS).

-I. SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAME CATION SUBFAMILY.
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Organic cation/carnitine transporter 2 (Solute carrier member 5) (High-affinity sodium-dependent carnitine cot SLC22A5 OR OCTN2.
 _MOUSE
 SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Kidney;
MEDLINE-99113835; PubMed-9916797;
MEDLINE-99113835; PubMed-9916797;
Nezu J., Tamai I., Oku A., Ohashi R., Yab
Nikaido H., Sai Y., Koizumi A., Shoji Y.,
Yashino M., Kato H., Ohura T., Tsujimoto
 Lu K., Nishimori H., Nakamura Y., Shima K., Kuwajima M.; "A missense mutation of mouse OCTNI, a sodium-dependent carnitine cotransporter, in the juvenile visceral steatosis mouse."; Biochem. Biophys. Res. Commun. 252:590-594(1998).
 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
 MEDLINE=99384224; pubMed=10454528; Wu X., Huang W., prasad P.D., Seth P., Chen J., Conway S.J., Ganapathy V.; "Functional characteristics and tissue
 SEQUENCE FROM N.A.,
STRAIN=C3H;
 cation transporter 2 (OCTN2), an organic
transporter.";
 MEDLINE=99057546; PubMed=9837751;
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 SEQUENCE FROM N.A.,
 "Primary systemic
 OCN2_MOUSE
 EMBL; AB015800; BAA36590.1;
EMBL; AF111425; AAC99787.1;
EMBL; AF110417; AAD54060.1;
MGD; MGI:1329012; Slc22a5.
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 mary systemic carnitine deficiency is caused by mutations encoding sodium ion-dependent carnitine transporter."; Genet. 21:91-94(1999).
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 Craniata; Vertebrata;
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 16-OCT-2001 (Rel. 40, Last annotation update) Organic cation/carnitine transporter 2 (Solutnember 5) (High-affinity sodium-dependent carn (UST2r) (CT1).
SLC22A5 OR OCTN2.
 "Functional characteristics and tissue distribution cation transporter 2 (OCTN2), an organic cation/carn transporter.";
 "Molecular cloning and characterization proteins from rat kidney."; FEBS Lett. 425:79-86(1998).
 SEQUENCE FROM N.A. TISSUE=Kidney;
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammmalia; Eutheria; Rodentia;
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 SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=99384224; PubMed=1045428;
Wu X., Huang W., Prasad P.D., Seth P., Rajan
Chen J., Conway S.J., Ganapathy V.;
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 Kanai Y., Endou H.;
"Molecular cloning and characterization of high-affinity transporter from rat intestine.";
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 MEDLINE-98200080;
 Pfam;
 SEQUENCE FROM N.A
 Biochem. Biophys. Res. Commun.
 Pharmacol. Exp. Ther. FUNCTION: SODIUM-ION
 SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN THE MYOCAMAL AND DISTAL TUBUL.
AND IN THE GLOMERULI IN THE KIDNEY, IN THE MYOCARDIUM, VALVES,
ARTERIOLES IN THE HEART, IN THE LABYRINTHINE LAYER OF THE
PLACENTA, AND IN THE CORTEX, HIPPOCAMPUS, AND CEREBELLUM IN TH
 Pharmacol. Exp. Ther. 290:1482-1492(1999).
FUNCTION: SODIUM-ION DEPENDENT, HIGH AFFINITY CARNITINE TUNCTIONS OF TRANSPORTS ORGANIC CATIONS WITHOUT THE INVOLVEMENT OF SODIUM. INVOLVED IN THE ACTIVE CELLULAR UPPORT OF SODIUM.
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 Kusuhara H., Utsunomiya-Tate N.,
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 al Similarity
476; Conser
 VYLGAYDRELPYILMGSLTILTAILTLEEPESEGAPLPDTIDQMLRVKGIKQWQIQSQTR
 431
489
57
64
91
275
 Metazoa; Nemat
e; Peloderinae;
 Conservative
 (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
(Rel. 32, Last annotation update)
1 84.8 kDa protein F23F12.5 in chromosome
 451
509
57
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275
62567
 STANDARD;
 Nematoda;
 87.
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N: Integral
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 oda; Chromadorea;
Caenorhabditis.
 42;
 POTENTIAL.

POTENTIAL.

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W -> G (IN REF. 2).

W -> G (IN REF. 2).
 Score
Pred.
 EMBL/GenBank/DDBJ databases.
 PRT;
 Mismatches
 e 2509; DB 1;
. No. 3.3e-153;
ismatches 39;
 751
 AA
 Rhabditida
 CRC64
 Length
 Indels
 (POTENTIAL).
(POTENTIAL).
 Rhabditoidea;
 557;
 0;
 Gaps
 300
 180
 180
 60
 480
 480
 420
 360
 360
 300
 240
 420
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YMP3_CAEEL
Q10947;
01-OCT-1996
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 Hypothetical TRANSMEM
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 Pfam;
 InterPro; IPR002184; Srb.
InterPro; IPR003662; sub_transporter.
Pfam; PF02175; Srb; 1.
 WormPep; F23F12.5;
 EMBL; U12965; AAA20607.1;
 TRANSMEM
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 656
 478
 363
 186
 303
 127
 363
 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
 TIVTEWNLVC-EDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRKNVLFVTMGNQTGFSF
 ASGFAPSWEVFAAFRFIVGTSIASILIVFYAYILEFIEPEQRVFLRS----FFNWGYAR
 MQLVPP
 LVFTLACFICGYWRSAAIATSLLSLPILPVLLILPESPKWFNTKKRFRDARAAEKRVAWL
 LQIFSKNFEMFVVLFVLVGMGQISNYVAAFVLGTEILGKSVRIIFSTLGVCIFYAFGY--
 SMVQDFKMFCGTKAYDAAWVATIQFIGVLIGAITYGHLGDHFGRKPVSFFGISVGILFGV
 LLARTGALLAPQMAYLSDIYRPAPYAVVCSIGTISLLISCVFLPDTKGVDL
 TASRLGSILSPYFVYLGAYDRFLPYILMGSL-TILTAILTLFLPESFGTPL
 LNSGNLAGNFYLSQFVSGAVTAFAKIFVFLLDTYVPSFDRRRLHQYPQIAMILCYCVIMV
 LDTPNLHGDIFVNCFLSAMVEVPAYVLAWLLLQYLP----RRYSM--ATALFLGGSVLLF
 SGIPYVNDEDQSIEISEKLEEKSTKIYTMKDLFTSWTIAYRTIVVGSLWFSTSLSAFGSD
 NGIVVPSTIFDPSELQD-LSSKKQQSHNILDLLRTWNIRMVTIMSIMLWMTISVGYFGLS
 MVLPLFAYFIRDWRMLLVALTMPGVLCVALWWFIPESPRWLISQGRFEEAEVIIRKAAKA
 LMILPESDCGSQGSRDLAII--IINIIGVSFIEITWDACYLVAVECFPTKIRTIGIGTCS
 PF00083; sugar_tr; 1
 Similarity
 24
57
102
137
200
235
320
320
348
379
379
410
432
515
515
515
5147
5147
 Conservative
 protein;
 A,
 STANDARD;
 34, Created)
 --DLYYLATVLVMVGKFGVTAAFSMVYVYTAELYPTVVRNMGVGVSS
 CE01252.
 84832 MW;
 13.4%;
25.8%;
 Transmembrane
 , 68
 Score 387.5;
Pred. No. 1e
 POTENTIAL.
POTENTIAL.
POTENTIAL.
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 POTENTIAL.
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 A6C4F43540295EFC CRC64;
 Mismatches
 387.5; DB 1;
No. 1e-17;
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 189;
 Length
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 517
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WormPep; bv...pfam; PF00083;
 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
 01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 139.9 kDa protein B0361.3 in chr
B0361.3.
 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
 khabditidae; Peloderinae;
NCBI_TaxID=6239;
 Eukaryota; Metazoa;
Rhabditidae; Pelode
 EMBL; U00031; AAK18864.1; -.
 Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases
 Caenorhabditis elegans
 -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 DPDKFVEAYGAYGKYQIFTYVLVQTL----NFFYSSSMYIMSFVQLNLEKQCE-----
 WMTISVGYFGLSLDTPNLHGDIFVNCFL-SAMVEVPAYVLAWLLLQYLPRRYSM-----
 PIIVTTAILAFLANMAASFSPNFAIFLILRAFIGACSDSYLSVASVATCEYLSEKAR-AW
 NVLFVTMGMQTGFSFLQIFSKNFEMFVVLFVLVGMGQISNYVAAFVLGTEILGKSVRIIF
 FSQDVYL-----STIVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRK 170
 DYDEVTAFLGEWGPFORLIFFLLSASIIPNGFTGLSSVFLIA----TPEHRCRVPDAANL
 EEAEVIIRKAAKANGIVVPSTIFDPSELQDLSSKKQQSHNILDLLRTWNIRMVTIMSIML
 ITVVYNVAWSLGMVWTLLVTLMTDDWRWRYFIVSLPGVYGFALWYFLPESPHWLITKNKT
 IAENTLVNVTNQKASTNLLVDFDLSCSHWFFQEFGLTIFTIGAVIAVPFMSMLADRYGRK
 ---YKNETIP-----ISETCQ---
 SSAWRNHTVPLRLRDGREVPHSCRRYRLATIANFSALGLEPGRDVDLGQLEQESCLDGWE
-MVISLVYFAISFMSVELGGD-QVQAFLYSSLIEIPAGLAVIPLMMKMGRKMIVIWCLVF
 al Similarity
118; Conserv
 в0361.3;
 Conservative
 sugar_tr;
 AA;
 CE00752.
 168
202
252
253
283
327
349
375
402
433
 Nematoda; Chromadorea; rinae; Caenorhabditis.
 12.4%;
21.1%;
 139868
 Transmembrane
 106;
 Score 357; DB
Pred. No. 1.5e
06; Mismatches
 MW;
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 POTENTIAL
 CBA42A80A254FB80 CRC64;
 -----IETESSKAFGNLNGEYC----G
 There are no rest
 DB 1;
L.5e-15;
 chromosome
 Rhabditida; Rhabditoidea;
 Usage
 Length 1222;
 Indels 126;
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 p30638; Q21101;
01-APR-1993 (Rel. 25, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 58.3 kDa protein ZK637.1 in chrop
 TRANSMEM
DOMAIN
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DOMAIN
 TRANSMEM
DOMAIN
 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-92168156; PubMed=1538779;
Sulston J., Du Z., Thomas K., Wilson R., Hillier
Halloran N., Green P., Thierry-Mieg J., Qiu L., D
Craxton M., Durbin R.K., Berks M., Metzstein M.,
Ainscough R., Waterston R.;
"The C. elegans genome sequencing project: a begi
 InterPro; IPR003662; sub_transporter.

Pfam; PF00083; sugar_tr; 1.

PROSITE; PS00216; SUGAR_TRANSPORT_1; FALSE_NEG.

PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.
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 Nature
[2]
 PIR; S15786; S15786. WormPep; ZK637.1; CE
 NCBI_TaxID=6239;
[1]
 Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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 Durbin R.;
 STRAIN-BRISTOL
 Caenorhabditis elegans
 TRANSMEN
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 Hypothetical
 477
 464
 364
 404
 send an email to license@isb-sib.ch).
 ; Z11115; CAA77460.1; ; Z22175; CAA77460.1; ; Z22175; CAA80131.1; ; Z211115; CAA80131.1;
 L-----
 MLRVKGMKHRKTPSHTRML
 SLMNIPQSMGIIMSPYVKHIVMSPNWIPFVVIALFSFISATLAFMLHETKNKKLPTDIES
 GVSSTASRLGSILSPYFVYLGAYDRFLPYILMGSLTILTAILTLFLPESFGTPLPDTIDQ
 QTLALIGVTVFL-----DSYEFKLVIMLVAKVMATIIYSVHPIWATEQFPTSVRSLCF
 ATALFLGGSVLLFMQLVPPDLYYLATVLVMVGKFGVTAAFSMVYVYTAELYPTVVRNMGV
 CAEEL
 . elegans genome sequencing
356:37-41(1992).
 1
86
107
121
142
158
179
180
201
 ---SYPSETNDL
 protein;
 .1; CE06638
 N2;
 STANDARD;
 106
120
141
141
157
178
179
208
 Nematoda;
 Transmembrane; Transport
 486
 542
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 JOINED
 Caenorhabditis
EXTRACELLULAR (POTENTIAL).
2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
 CYTOPLASMIC
 Chromadorea;
 PRT;
 (POTENTIAL)
 529
 (See http://www.isb-sib.ch/announce/
 There are no restrictions ong as its content is in
 chromosome
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 Rhabditida; Rhabditoidea;
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NCBI_TaxID=562;
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 TRANSMEM
 460
 463
 404
 405
 344
 185
 105
 311
 197
 125
 146
 369
 291
 232
 255
 8
 10
 al Similarity
140; Conser
 462
481
483
503
529
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...vv-1997 (Rel. 35, Created)
01-MAR 2002 (Rel. 41, Last annota
Hypothetical metabolite trans^^
YGCS OR B2771.
Escherichia
Bacteria; Proteobacteria; Escherichia.
 52 VPDAANLSSAWRNHTVPLRLRDGREVPHSCRRYRLATIANFSALGLEP -- GRDVD-----
 VGVSSTASRLGSILSPYFVYLGAYDRFLPYILMGSLTILTAILTLFLP
 TICVESGMMLSSTEWGKICDREGRRKGLTESTLVACIMGVISGMSPHEYVLLEFRGLTGE
 VLEASNLTEAYVDLTAKQLIKEIRHVGDDF-AVRYSNLDDRTELG-EFTDQRSPDSEKTF
 T--ALFLGGSVLLEMQLVPPDLYYLATVLVMVGKFGVTAAFSMVYVYTAELYPTVVRNMG
 FQSHDECHGGLFSNGTQMEVCQPLTRSDYFDLLSTTLAEFPGLIITVLIIEWFGRKKTMA
 TIFDPSELQDLSSKKQQSHNILDL--LRTWNIRMVTIMSIMLWMTISVGYFGLSLDTPNL
 ESFGWRALMFLSSLPLGIFAVASFW-LPESARFDMASGHPERALETLQAAARMNRVQLPT
 TVDEAVEALGFGRFQLKLSILTGMAWMADAMEMMLLSLISPALACEWGI---SSVQQALV
 -------LGQLEQE-SCLDGWEFSQD----VYLSTI----VTEWNLVCEDDWKAPLT
 LGTCSAMARIGAIVA----
 VVLFVLVGMGQISNYVAAFV--LGTEILGKSVRIIFSTLGVCIFYAFGYMVLPLFAYFIR
 ISLFFVGVLLGSFISGQLSDRFG-RKNVLFVT-----MGMQTGFS--
 -GIGGVPQSVTLYAEFLPTAQRAKCVVLIES-----FWAIGAVFEALLAYFVM
 HGDIFVN----
 Conservative
 -RLVSSTKAGSESRGDIANLLSPDLRKTTILLWCIWAITAFSYYGMVLFTTVL
 STANDARD;
 237
258
319
340
372
393
410
431
431
455
461
461
480
480
58317
 12.3%;
 Last sequence up
 transport
 -SEKSLSLPIGIYGTAAILGLIASLSLP
 MW;
 gamma
 97;
 EXTRACELLULAR (POTENTIAL)
10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
12 (POTENTIAL).
 Score 355.5;
Pred. No. 7.
 EXTRACELLULAR (POTENTIAL).
6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
 CYTOPLASMIC
 CYTOPLASMIC (
9 (POTENTIAL)
 EXTRACELLULAR 8 (POTENTIAL).
 PRT;
 TOPLASMIC (POTENTIAL).
8D2FF4CBA15ECD2D CRC64
 subdivision;
 Mismatches
 ---CFLSAMVEVPAYVLAWILLQYLPRRYSMA
 protein
 update)
 445
 update)
 .7e-16;
 B
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 ygcs
 DB 1; Length
 (POTENTIAL)
 186;
 Enterobacteriaceae;
 Indels
 FLQIFSKNFEMF
 510
 529;
 105;
 Gaps
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 DOMAIN
TRANSMEM
 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
 SEQUENCE FROM N.A. STRAIN-K12 / MG1655; MEDLINE-97426617; PubMed-9278503;
 TRANSMEM
DOMAIN
 pfam; PF00083; sugar_tr; 1.
proSITE; pS00216; SUGAR_TRANSPORT_1;
proSITE; pS00217; SUGAR_TRANSPORT_2;
 EMBL; U29579; A EMBL; AE000360;
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 Mau B.,
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A.,
 Blattner F.R., Plunkett G. III, Bloch C.A., Perna Riley M., Collado-Vides J., Glasner J.D., Rode C.
 TRANSMEM
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 Complete
 Hypothetical protein;
 EcoGene; EG13126;
 SEQUENCE
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 TRANSMEM
 InterPro; IPR003662; sub_transporter
 TRANSMEM
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 FRANSMEM
 151
 SIMILARITY: BELONGS TO
 SUBCELLULAR LOCATION: Integral membrane protein.
 (Potential)
 VGVLLGSFISGQLSDRFGRKNVLFVIMGMQTGFSFLQIFSKNFEMFVVLFVLVGMGQISN
 LPALLITLLRWGTPESPRWLLRQGRFAEAHAIVHR----
 MPGVLCVALWWFIPESPRWLISQGRFEEAEVIIRKAAKANGIVVPSTIFDPSEL--QDLS
 YSVGHTLLAEFSPRRHRGIL--LGAFSVVWTVGYVLASIAGHHFISENPEAWRWLLASAA
 YVAAFVLGTEILGKSVRIIFSTLGV-CIFYAFGYMVLPLFA-YFIRD---
 {\tt LGLFLGSLVLGWISDHIGRQKIFTFSFLLITLASFLQFFATTPEHLIGLRILIGIGLGGD}
 102;
 Shao Y.;
 Similarity
 proteome
 Conservative
 AAA69281.1; ALT_INIT.
0; AAC75813.1; ALT_INIT.
 ygcs
 48234
 10.7%;
 Transport;
 M
 THE SUGAR TRANSPORTER FAMILY.
 8 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
 2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
 79;
 Score 308; DB Pred. No. 6.9e
 CYTOPLASMIC
11 (POTENTIA)
 CYTOPLASMIC (POTENTIAL); B59E452721B15774 CRC6
 CYTOPLASMIC
 PERIPLASMIC (
4 (POTENTIAL)
 CYTOPLASMIC
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 Transmembrane; Inner
 FALSE_NEG
 DB 1;
.9e-13;
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 Perna N.T., Burland V., ode C.K., Mayhew G.F.,
 168;
 Length 445;
 Indels
YFGPHVLLGDEVV
 Inner membrane
 Rose D.J.,
 membrane;
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01-OCT-1996
01-OCT-1996
 TRANSMEM
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SEQUENCE
 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 use by non-profit institutions as long modified and this statement is not removed
 Q10917;
 entities requires a license agreement (S or send an email to license@isb-sib.ch).
 the European Bioinformatics Institute. The Three by non-profit institutions as long
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 Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
 Du
 Hypothetical 48.6
 Pfam; PF00083; sugar_tr; 1
 STRAIN-BRISTOL N2;
 NCBI_TaxID=6239;
 Hypothetical protein;
TRANSMEM 55 7
 InterPro;
 WormPep;
 EMBL; U23453; AAC46757.1; -.
 SEQUENCE FROM N.A
 407
 496
 288
 323
 128 IVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRKNVLFVTMGMQTGFSFLQ
 151
307
 210
 248
 188
 91
 Local
 Z., Waterston
 _CAEEL
 ATVLLVGFVVTWLWAPETKALPL 429
 GSLTILTAILT-LFLPESFGTPL
 TISAVSNLVGILPAESFPTDIRSLGVGFATAMSRLGAAVSTGLLPWVLAQWGMQVTLLLL 406
 GVTAAFSMYYYYTAELYPTVVRNMGYGVSSTASRLGSILSPYFV--YLGAYDRFLPYILM 495
 MENALLIVGALLG-LVLTHLLAHRKFILGSFLLLAATLVVMACLPSGSSLTLLLFVLFST
 EVPAYVLAWLLLQYLPRRYSMATALFLGGSVLLF-----MQLVPPDLYYLATVLVMVGKF
 TATHKHIKTLFSSRYWR----RTAFNSVFFVCLVIPWFVIYTWLPTIAQTIGLEDALTASL
 SKKQQSHNILDLLRTWNIRMVTIMSIMLWMTISVGYFGLSLDTPNLHGDIFVNCFLSAMV 382
 VADEFDLTGDASWLAESTTTFYMVGNMIGGMFIPPLADHYGRLFVFVATVLLMAVGGMIS
VVPSTIFDPSELQDLSSKKQQSHNILDLLRTWNIRMVTIMSIMLWMTISVGYFGLSLDTP
 LLAYILPDWRYLMFCISVPNIFVALLIYMTVPESLHFLVSSQQNEKIEAWLEKIRGPKGD
 LFAYFIRDWRMLLVALTMPGV-LCVALWWFIPESPRWLISQGRFEEAEVIIRKAAKANGI
 AFSTSIMMFCIMRMIHGIFYTAAGLAGWVLGYENTPLRLR-FFTSVYFGVMWVVGACFLG
 IFSKNFEMFVVLFVLVGMGQISNYVAAFVLGTEILGKSVRIIFSTLGVCIFYAFGYMVLP
 90;
 Similarity
 B0252.3; CE02419
 IPR003662;
 384
435 AA;
 (Rel. 34, Creaceu,
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
(Rel. 34, Last annotation update)
1 48.6 kDa protein B0252.3 in chromosome
 Conservative
 STANDARD;
 404
48571 MW;
 75
 10.1%;
21.5%;
 sub_transporter
 Transmembrane
 78;
 517
 Score 291.5;
Pred. No. 7.
 POTENTIAL.
: 5F6160359FA1840B CRC64;
 POTENTIAL.
 PRT;
 Mismatches
 435
 (See http://www.isb-sib.ch/announce/
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 ere are no rest
 DB 1;
 Usage
 Length 435;
 Indels
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 restrictions
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 a collaboration
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MBL outstation
 83;
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 Gaps
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 346
 366
 209
 150
 247
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RESULT 9
YCEL_BACSU
ID YCEL_BACSU
AC 034691
DT 30-MAY
DT 10-MAR
DE YCEL.
OS Bactlal
OC Bactlal
OC Bactlal
OC STRAIN
RA KUMBAIC
RT 16ABIL;
RA SEDUEN
RA CUBBAIC
RT 16ABIL;
CC -1- SI
CC DETMES
CC TILL
CC DETMES
CC DETMES
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 Kumano M., Tamakoshi A., Yamane K.;

"A 32 kb nucleotide sequence from the region of the lincomycin-
resistance gene (22-25 degree) of the Bacillus subtills chromose
identification of the site of the lin-2 mutation.";

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 SubtiList; BG12773; yceI.
InterPro; IPR003662; sub_transporter.
 TRANSMEM
 TRANSMEM
 DOMAIN
 TRANSMEM
 DOMAIN
 TRANSMEM
 Hypothetical
DOMAIN
 Pfam; PF00083;
 entities requires
 STRAIN-168;
 SEQUENCE FROM N.A.
 Bacillus subtilis.
Bacteria; Firmicutes; Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID=1423;
 Hypothetical YCEI.
 30-MAY-2000
01-MAR-2002
 CEI_BACSU
 381
 426
 293
 367
 tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
) ISASDI---
 AB000617; BAA22256.1; 299105; CAB12089.1; -
 VHALAPAITLSLIAVSGGLLTLILPETLNTKLPSTI----
 YLATVLVMVGKFGVTAAFSMYYVYTAELYPTVVRNMGVGVSSTASRLGSILSPYFVYLGA
 YDRFLPYILMGSLTILTAILTLFLPESFGTPLPDTIDQMLRVKGMKHRKTPSHTRMLKD
 ----IKTEKTTLEQDRRYIYLEWI-----
 NLHGDIFVNCFLSAMVEVPAYV-LAWLLLQYLPRRYSMATALFLGGSVLLFMQLVPPDLY
 PS00216;
PS00217;
 00 (Rel. 39, Createu,
00 (Rel. 39, Last sequence upda
02 (Rel. 41, Last annotation u
15
36
50
71
71
78
99
120
143
1164
1166
1187
2188
2399
281
 protein;
 sugar_tr; 1.

1.16; SUGAR_TRANSPORT_1; FALSE_NEG.

117; SUGAR_TRANSPORT_2; 1.

20 TOTEIN: Transport; Transmembrane;

20 TOTEIN: AMTC (POTEN)
 HEFGRSSSLHFFSDFHEQIFPTDGRNKCIGFCETLSRFGGMLSPYLSHLTA
 STANDARD;
-VEDRDENGSSFKTLCRE-
 Bacillus/Clostridium
 group;
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 3 (POTENTIAL).
4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC
9 (POTENTIAL
 EXTRACELLULAR (POTENTIAL) 8 (POTENTIAL).
 EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Gregor J., Davis N.W., Mau B., Shao Y.;
 MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado Vides J., Glasner J.D., R
 Nucleic
[2]
 Isono K., Mizobuchi K., Nakata "Systematic sequencing of the E the 0-2.4 min region.";
 SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; Pu
 01-JUL-1993 (Rel. 26, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Hypothetical metabolite transport prot
YAAU OR B0045.
 YAAU_ECOLI
P31679; P31578;
 TRANSMEM
DOMAIN
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 MEDLINE=92334977; PubMed=1630901;
 SEQUENCE
 Escherichia
 Bacteria;
 Escherichia
 330
 452
 273
 393
 214
 340
 281
 116 GWEF-SQDV-YLSTIV----TEWNLYCED-DWKAPLTISLFFYGYLLÇSFISGQLSDRFG
 189
 169
 75
 19
 Match
Local Similarity
 EQYPTAIRATGSGTTAAFGRIGGIFGPLLVGTLAA--RHISFSVIFSIFCIAILLAV
 ELYPTVVRNMGVGVSSTASRLGSILSPYFV-YLGAYDRFLPYILMGSLTILTAILTL
 KSVRIIFSTLGVCIFYAFGYMVLPLFAYFI---RDWRMLLVALTMPGYLCVALWWFIPES
 RKNVLEVIMGMQIGFSFLQIFSKNFEMFVVLFVLVGMGQISNYVAAF\LGTEIL-----
 LIEKAGRKWILVVYLIGTAGSAYFFG--TADSLSLLLTAGVLLSFFNL-GAWGVLYAYTP
 LLQYLPRRYSMATALF-LGGSVLLFMQLVPPDLYYLATVLVMVGKFGVTAAFSMVYVYTA 451
 PRWLISQGRFEEAEVIIRKAAKANGIVVPSTIFDPSELQDLSSKKQQS-HNILDLLRTWN
 RKKVFIITLLCFSIGSGISAFVTSLSAFLILRFVIGMGLGGELPVAS†LVSEAVVPEKRG
 GWLFDAMDVGILSFIIAALHVEWNLSPEEMKWIG----SVNSIGMAAGAFLFGLLADRIG
 IRPTYMLSI-VWFCVVFSYYGMFLWLPSVMLLKGFSMIQSFEYVLLM†LAQLPGYFSAAW
 IRMVTIMSIMLWMTISVGYFGLSLDTPN---LHGDIFVNCF----LSאַאVEVPAYVLAWL
 RVIVLLES-----FWAVGWLAAALISYFVIPSFGWQAALLLTALTAFYALYLRTSLPDS
 104;
 Acids
 FROM N.A.
 Proteobacteria;
 coli
 400
 Conservative
 302
305
326
344
365
371
392
 STANDARD;
 A
 P75628;
 20:3305-3308(1992)
 304
325
343
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370
391
 43708
 10.0%;
 Kirkpatrick H.A.,
 gamma
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 76;
 Nagata
 EXTRACELLULAR (POTENTIAL).

10 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

11 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

12 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

E0AEOCEESDD27395 CRC64;
 Score 287; DB
Pred. No. 1.4e
76; Mismatches
 Escherichia
 PRT;
 subdivision; Enterobacteriaceae;
 protein
 Т.,
 update)
 443
 update)
 ----ESLSAKKRSMWENVKSVWARQY
 Ishihama
 DB 1;
1.4e-11;
 Goeden M.A.,
 A
 Rode C.K
 coli
 yaaU
 161;
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 TRANSMEM
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 Complete
 EMBL;
 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inne
 DOMAIN
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 DOMAIN
 Pfam; PF00083;
 EcoGene; EG11566;
 PIR; S40566; S40566
 DOMAIN
 TRANSMEM
 Hypothetical protein;
103 VSSPVELLVMRVLIGIVIGADYPIATSMITEFSSTRQR-AFSISFIAAMWYVGATCADLV
 48
 SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO IN POSITION 142 AND 232 THAT PRODUCE TWO SEPARATE ORFS.
 (Potential).
 LVCEDDWKAPLTISLFFVGVLLGSFIS----GQLSDRFGRKNVLFVTMGMQTGFSFLQIF
 SKNFEMFVVLFVLVGMGQISNYVAAFVLGTEILGKSVRIIFSTLGVCIFYAFGYMVLPLF
 D10483; BAA01321.1;
 AE000114;
 Similarity
 00083; sugar_tr; 1.

PS00216; SUGAR_TRANSPORT_1; FALSE_NEG.
PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.
PS00217; STORT Transport; Transmembrane;
 proteome.
 PR003662;
 19
40
54
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106
 AA;
 AAC73156.1;
 ~IGLLGAGTLAGLFVGTSLFGYISDKVGRRKMFLIDIIAIGVISVATMF
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2 (POTENTIAL).
12 (POTENTIAL).
13 (POTENTIAL).
14 (POTENTIAL).
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 ALT_FRAME
 Integral membrane protein. Inner
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CYTOPLASMIC (P
 6 (POTENTIAL).
CYTOPLASMIC (P.
 Score
Pred.
 8 (POTENTIAL).
CYTOPLASMIC (F
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 CYTOPLASMIC
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 CYTOPLASMIC
1 (POTENTIAL
 5 (POTENTIAL)
PERIPLASMIC (
 PERIPLASMIC
2 (POTENTIAL
 CYTOPLASMIC
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10 (POTENTIA
 PERIPLASMIC
 (POTENTIAL)
 AEF484D8B109DE05
 (POTENTIAL)
 Mismatches
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 SIH -> L (IN REF. 1).

SIH -> CLHY (IN REF. 1).

Y (IN REF. 1).

Y (IN REF. 1).

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 267; DB 1;
No. 2.9e-10;
 REF.
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 CRC64;
 Length 443;
 Inner
 Indels
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 EMBL
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 Gaps
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RESULT
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 P76230; P76911;
15-JUL-1999 (Rel. 38, 0
15-JUL-1999 (Rel. 38, 1
01-MAR-2002 (Rel. 41, 1
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 _ECOLI
YDJK_ECOLI
 Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yanamoto Y., Horiuchi T., Tako DNA Sequence of the Escherichia coli K-12 Genome Corresponding to the 28.0-40.1 min Region on the Linkage Map. DNA Res. 3:363-377(1996).
 This
 Science
 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Ma Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., R
 STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
 MEDLINE=97251357;
 STRAIN-K12
 SEQUENCE FROM N.A.
 Escherichia
 Hypothetical r
YDJK OR B1775
 +
 NCBI_TaxID=562;
 Bacteria;
 "The
 EQUENCE FROM N.A.
 528
 381
 472
 321
 417
 275
 361
 216
 250
 440 QRM
 В.,
 ween the Swiss Institute of Bioinformatics Institute.
 SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 SUBCELLULAR LOCATION: Integral membrane protein.
 SWISS-PROT entry is
 (Potential)
 KGM
 complete genome sequence complete genome sequence 277:1453-1474(1997).
 IGTIVSTWALPIFINNYG-ISNTMLMGAGISLFGLLISVAFAPETRGMSLAQTSNMTIRG
 {\tt LALAVLGLIPDMGIWLVVMAFAVYAFFSGGPGNLQWLYPNELFPTDIRASAVGVIMSLSR}
 IVVPSTIFDPSELQ-----DLSSKKQQSHNILDLLRTWNIRMVTIMSIMLWMTISVGYFG
 GYWLYDVEGGWRWMLGSAAIPCLLILIGRFELPESPRWLLRKGRVKECEEMMIK-----
 AYFIRD----WRMLLVALTMPGVLCVALWWFIPESPRWLISQGRFEEAEVIIRKAAKANG
 LGSILSPYF -- VYLGAYDRFLPYILMGSLTILTAIL -- TLFLPESFGTPLPDTIDQMLRV
 MQLVPPDLYYLATVLVMVGKFGVTAAFS-----MVYVYTAELYPTVVRNMGVGVSSTASR
 LSLDTPNLHGDIFVNCFLSAMVEVPAYVLAWLLLQYLPRRYSMATA----LFLGGSVLLF
 LFGEPVAFDEEQPQQTRFRDLFNRRHFPF-VLFVAAIWTCQVIPMFAIYTFGPQIVGLLG
 Shao Y.;
 530
 Proteobacteria;
 coli
 metabolite transport protein
 STANDARD;
 PubMed=9097039;
 Institute of Bioinformatics and the EM
 Last sequence update)
Last annotation updat
 Created)
 gamma
 of
 subdivision; Enterobacteriaceae;
 Escherichia coli K-12.";
 -FMLGCIPPMLWLNTAGRRPLLIGSFAMMT
 459
 update)
 Goeden M.A., Rose
 ydjK.
 C.K., Mayhew G
 Inner membrane
 restrictions
 T., Saito
 Burland V.,
 a
 D.J.,
 collaboration -
 Itoh
 'n
 439
 471
 380
 320
 274
 360
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Query Match
Best Local S
Matches 101
 DOMAIN
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SEQUENCE
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 Hypothetical
Complete prot
 EMBL; AE000272; AAC74845.1; -.
EMBL; D90821; BAA15573.1; ALT_INIT
EcoGene; EG13487; ydjK.
 SYV2_RAT
 DOMAIN
 TRANSMEM
 DOMAIN
 PROSITE;
 Pfam; PF00083;
 DOMAIN
 TRANSMEM
 152
 12
 LQDLSSKKQQSHNILDLLRTWNIRMVTIMSIMLWMTISVGYFGLSLDTP-----
 VAAFVLGTEIL-GK----
 GMFLGALVGGIIGDKTGRRNAFILYEAIHIASMVVGAFSPNMDFLIACRFVMGVGLGALL
 GVLLGSFISGQLSDRFGRKNVLFVIMGMQTGFSFLQIFSKNFEMFVVLFVLVGMGQISNY
 AVLLSSYGVTGVFILLGAVSIIVAI
 FVYLGAYDRFLPYILMGSLTILTAI
 TSMLLITLIGFFLITFVYMYVCYASAVYVPEIWPTEAKLRGSGLANAVGRISGIAAPYAV
 T---VLVMVGKFGVTAAFSMV----YVYTAELYPTVVRNMGVGVSSTASRLGSILSPY--
 DSIVLNIM--SMFGAPFGIFIAMLVMDKIPRK-IMGVGLLILIAVLGY-----
 GDIFVNCFLSAMVEVP-AYVLAWILLQYLPRRYSMATALFLGGSVLLFMQLVPPDLYYLA
 LTMPGVLCVAL-WWFIPESPRWLISQGRFEEAEVIIRK----AAKANGIVVPSTIFDPSE
 VTLFAGFTEYMPGRNRGTWSSRVSFIGNWSYPLCSLIAMG--LTPLIS-AEWNWRVQLLI
 IAD-DGKAPQAVPYSALLTGVLLKRVILGSCVL-IAMNVVQYTLINWLPTIFMTQGINLK
 PAILSLIATALAWRYFPESPRWLESRGRYQEAEKVMRSIEEGVIRQTGKPLP-----PVV
 101;
 Similarity
 proteome
 IPR003662; sub_transporter.
0083; sugar_tr; 1.
ps00216; SUGAR_TRANSPORT_1; FALSE_NEG.
ps00217; SUGAR_TRANSPORT_2; FALSE_NEG.
cal protein; Transport; Transmembrane;
 PS00217;
 Conservative
 STANDARD;
 49602
 9.2%;
 ·SVRIIFS---TLGVCIFYAFGYMVLPLFAYFIRDWRMLLVA
 ₩;
 4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
5 (POTENTIAL)
 2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
 79;
 Score 265; DE
Pred. No. 4e-1
'9; Mismatches
 9 (POTENTIAL).

PERIPLASMIC (P
10 (POTENTIAL)

CYTOPLASMIC (P)
11 (POTENTIAL)

12 (POTENTIAL)
 7 (POTENTIAL)
PERIPLASMIC (F
8 (POTENTIAL)
CYTOPLASMIC (F
9 (POTENTIAL)
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PERIPLASMIC (F
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CYTOPLASMIC (F
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BC8AB53ECB8BDD77 CRC64;
 3 (POTENTIAL)
PERIPLASMIC (
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 153;
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 Length 459
 Inner
 Indels
 membrane;
 52;
 -IYSLQ
 -NLH
 Gaps
 241
 317
 186
 349
 18;
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Best Local
 Q02563;
01-FEB-1995
01-FEB-1995
30-MAY-2000
 Synaptic
SV2
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CARBOHYD
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TRANSMEM
 use by non-profit institutions as lo modified and this statement is not remo entitles requires a license agreement (or send an email to license@isb-sib.ch)
 Science 257:1271-1273(1992).

-!- FUNCTION: WAY ACT AS A VESICLE-LOCALIZED NEUROTRANSMITTER TRANSPORTER OR MAY FUNCTION AS AN ION TRANSPORTER OR CHANNOTS USUAL LOCATION: SYNAPTIC VESICLE.
-!- TISSUE SPECIFICITY: NEURAL AND ENDOCRINE CELLS OF BRAIN AN SPINAL CORD.
 between the Swiss Institute of Bioinformatics Institute.
 This
 MEDLINE=92390722; PubMed=1519064;
Bajjalieh S.M., Peterson K., Shingal R., Scheller
"SV2, a brain synaptic vesicle protein homologous
transporters.";
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 SEQUENCE
 TRANSMEM
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 Transmembrane.
 Synapse;
 Pfam;
 TISSUE=Brain;
 SEQUENCE FROM N.A.,
 NCBI_TaxID=10116;
 Rattus norvegicus (Rat).
 DOMAIN
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 Local Similarity nes 115; Conserv
 96 GLEPGRDVDLGQLEQESCLDGWEFSQDVYLSTIVTE-----
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 PF00083;
 L05435; AAA42188.1;
 995 (Rel. 31, Created)
995 (Rel. 31, Last sequence update)
900 (Rel. 39, Last annotation update)
vesicle protein 2 (SV2).
 Nerve;
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 Glycoprotein;
 Chordata;
Rodentia;
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CYTOPLASMIC (POTENTIAL).
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 Score 262.5;
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RESULT 1
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(POTENTIAL)

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D50543; BAA09111.1; -. Z99108; CAB12655.1; -.

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01-OCT-1996
01-MAR-2002
 YFIG_BA(
P54723;
 LT 13
_BACSU
 "Determination of a 12 kb nucleotide sequence around region of the Bacillus subtilis chromosome.";
Microbiology 142:1417-1421(1996).
-i- SUBCELLULAR LOCATION: Integral membrane protein
 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical metabolite transport protein yfic.
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 the
 between
 MEDLINE=96262713; PubMed=8704981;
 SEQUENCE
 Bacillus/Staphylococcus group;
NCBI_TaxID=1423;
 Bacteria; Firmicutes;
 Bacillus subtilis
 471
 582
 462
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 SUBCELLULAR LOCATION: Integral membrane protein (pro
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 KLAAVLGISIFTSFVG-----
 RLGSIL--SPYFVYLGAYDRFLPYILMGSLTILTAILTLFLPESFGTPLPDTIDQMLR 526
 SVFAFFSSFVQGYGTFLFCRLLSGVG-------IGGSIPIVFSYFSEFLAQE
 BACSU
 VSCFFLSFGNSESAMIA-LLCLFG--GVSIASWNALDVLTVELYPSDKRTTAFGFLNALC
 ---LEMQLVPPDLYYLATVLVMVGKFGVT-AAFSMVYVYTAELYPTVVRNMGVGVSSTAS
 GCPLDVTGTGEGAYMVYFVSFLGTLAVLPGNIVSALLMDKIGRLRMLA-----GSSVLSC
 YGLTVWFPDMIRHLQAVDYAARTKVFPGERVEHVTFNFTLENQIHRGGQYFNDKFIGLRL
 QEDELIEIQSDTGTWYQRWGVRALSLGGQVWGNFLSCFSPEYRRITLMMMGVWFTMSFSY
 VALWWFIPESPRWLISQGRFEEAEVIIRKA----AKANGIVVPSTIFDPSELQDLSSKKQ
 KRGEHLSWLCMFWMIGGVYAAAMAWAIIPHYGWSFQMGSAYQFHSWRVFVLVFAFPSVFA
 TGFSFLQIFSKNFEMFVVLFVLVGMGQISNYVAAFVLGTEILGKSVRIIFSTLG-----
 KSVSFEDSLFEECYFEDVTSSNTFFRNCTFINTVFYNTDLFEYKFVNSRLVNSTFLHNKE
 FGLSLDTPNL------
 QSHNILDL------LRTWNI-----
 IGALTTQPESPRFFLENGKHDEAWMVLKQVHDTNMRAKG--HPERVFSVTHIKTI----H
 VFVVGFVLPSAEKDMCLSDSNKGMLGLIVYLGMMVGAFLWGGLADRLGRRQCLLISLSVN
 GLSDGEGPPGGRGEAQRRKDREELAQQ--YETILRECGHGRFQWTLYFVLGLALMADGVE
 FROM N.A.
 -VCIFYAFG
 STANDARD;
 -VCEDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRKNVLFVTMGMQ
 Bacillus/Clostridium group;
 -FLSAMVEVPAYVLAWLLLQYLPRRYSMATALFLGGSVL--
 HGDIFVNC----
 ----YMVLPLF------AYFIRDWRMLLVALTMPGVLC
 -ITKAAPILFASAALALGSSLALKLPETRGQVLQ 742
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 SubtiList; BG11854; yfiG.
InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
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 Pfam; PF00083;
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MEDLINE=97251357; PubMed=9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Katai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Misobuchi K., Mori H., Mori T., Motomura K., Makino K., Miki T., Mashimoto H., Nishio Y., Oshima T., Saito Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takeuchi Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wadad C., Yamamoto Y., Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
DNA Res. 3:363-377(1996).
 Science [2]
 EMBL;
 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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 "Intrinsic and "";
bacterial genome.";
bacterial genome.";
Nucleic Acids Res. 22:4756-4767(1994).
Nucleic Acids Res. 10CATION: Integral membrane
 SEQUENCE FROM N.A.
STRAIR-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 TDJE_ECOLI STANDARD; PRT; 452 AA. p38055; P77244; O1-CCT-1994 (Rel. 30, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update) Hypothetical metabolite transport protein ydjE. YDJE OR B1769.
 ECOLI
 EMBL; D90821; BAA15567.1; -.
EMBL; M26934; -; NOT_ANNOTATED_CDS
ECoGene; EG12369; ydjE.
 Jerlstroem P.G., Bezjak D.A., Jennings M.P., Beacham I.R.; "Structure and expression in Escherichia coli K-12 of the L-asparaginase I-encoding ansA gene and its flanking regions."; Gene 78:37-46(1989).
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 SEQUENCE FROM N.A. STRAIN=K12;
 Bacteria;
 Borodovsky M.,
 MEDLINE-95075659; PubMed-7984428;
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IDENTIFICATION
 MEDLINE=89357501; PubMed=2670682;
 SEQUENCE OF 360-452 FROM N.A.
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 Escherichia
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 InterPro;
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 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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 D90821; BAA15567.1; M26934; -; NOT_ANNO
 AE000272;
D90820; B
 Pro; IPR003662;
PF00083; sugar_
 Proteobacteria;
 coli.
 BAA15560.1; -.
 Rudd K.E., Koonin E.V.;
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 84 YRLATIANFSALGLEPGRDVDLGQLEQESCLDGW-EFSODVYLSTIVTE-WNLVCEDDWK 141
 21
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 MVLPLEAYFIRDWRMLLVALIMPGVLCVALWWFIP----ESPRWLISQGRFEEAEVIIR
 WLIFFRFLMGTGMGALIMVGYASFTEFIPATVRGK----WSARLSFVGNWSPMLSAAIGV
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HLRLRGSGFVNAVGRIVAVFTPYGVAALLTHYGSITVFMVLGVMLLLQALVLSIF 436
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 KA----AKANGIVVPSTIFDPSELQDLSSKKQQSHNILDLLRTWNIRMVTIMSIMLWMTI
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 114;
 proteome.
 -LFGSTLLIIIAVLGYIYSIQTTEWAILIYGLVMIFFLYMYVCEASAVYIPELWPT
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 Score 255.5;
Pred. No. 1.
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InterPro; IPR003662; sub_t
Pfam; PF00083; sugar_tr; I
PROSITE; PS00216; SUGAR_TP
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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## SUMMARIES

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|--------------|--------|----------------|-----------------------|-----|--------|--------------------|
| _            | 2876   |                | 557                   | 4-  | Q96ЕН6 | Q96eh6 homo sapien |
| 2            | 2295.5 |                | 564                   | 11  | Q9WTN6 | Q9wtn6 mus musculu |
| ω            | 2227   |                | 551                   | 4   | Q9Н015 | Q9h015 homo sapien |
| 4            | 2218   |                | 551                   | 4   | 014546 | O14546 homo sapien |
| <sub>U</sub> | 2157   |                | 553                   | 11  | Q9R141 | Q9r141 rattus norv |
| 6            | 2148   |                | 553                   | 11  | Q9Z306 | Q9z306 mus musculu |
| 7            | 885    |                | 548                   | σı  | Q9VCA2 | Q9vca2 drosophila  |
| 8            | 881    |                | 548                   | G   | 001384 | 001384 drosophila  |
| 9            | 816    | 28.3           | 567                   | υ   | Q9VCA3 | Q9vca3 drosophila  |
| 10           | 811    |                | 567                   | σı  | Q95R48 | Q95r48 drosophila  |
| 11           | 799.5  |                | 577                   | 4   | Q96RU0 | Q96ru0 homo sapien |
| 12           | 777    |                | 568                   | ű   | Q9U539 |                    |
| 13           | 777    |                | 576                   | σ   | 002270 | 002270 caenorhabdi |
| 14           | 761.5  |                | 563                   | σı  | Q95TW6 | Q95tw6 drosophila  |
| 15           | 753.5  |                | 561                   | տ   | Q9V6L6 | Q9v616 drosophila  |
| 16           | 740    |                | 554                   | 4   | Q9NQD4 | Q9nqd4 homo sapien |
|              |        |                |                       |     |        |                    |

| 45                 | 44                 | 43     | 42                 | 41                 | 40                 | 39                 | 38     | 37                 | 36     | 35     | 34                 | 3<br>3             | 32                | 31                 | 30                | 29                 | 28                | 27                 | 26                 | 25                 | 24                 | 23                 | 22                 | 21                 | 20     | 19     | 18     | 17                 |
|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|
| 660.5              | 661.5              | 675.5  | 675.5              | 681.5              | 688.5              | 690                | 690.5  | . 693              | 703    | 703.5  | 704                | 709                | 709.5             | 710                | 711               | 714.5              | 716.5.            | 718                | 723.5              | 724                | 727                | 728                | 728                | 733                | 734    | 735.5  | 738    | 738.5              |
|                    | 22.9               |        |                    |                    |                    |                    |        |                    |        |        |                    |                    |                   |                    |                   |                    |                   |                    |                    |                    |                    |                    |                    |                    |        |        | 25.6   |                    |
| 456                | 537                | 562    | 553                | 551                | 551                | 548                | 551    | 542                | 551    | 539    | 556                | 556                | 604               | 535                | 554               | 553                | 674               | 556                | 554                | 555                | 555                | 593                | 557                | 593                | 554    | 540    | 554    | 556                |
| 4                  | 11                 | 13     | 4                  | 11                 | 11                 | 4                  | 11     | 4                  | 4      | 4      | 11                 |                    |                   | 11                 | 0                 | 11                 | ഗ                 | 11                 | σ                  | 11                 | 4                  | 1                  | 4                  | 11                 | 4      | 11     | 4      | 4                  |
| 014567             | Q91WJ9             | 057379 | Q96S37             | 088446             | Q99JF0             | Q9Y694             | Q9WTW5 | Q96TC1             | Q9Y226 | Q9H2W5 | Q9R1Q4             | 008966             | Q961J5            | Q63314             | 002713            | 070577             | Q9VIK2            | Q63089             | 077504             | Q9R0W2             | 015244             | P97558             | Q96KH7             | P70485             | 015245 | Q91WU2 | 015395 | 075751             |
| 014567 homo sapien | Q91wj9 mus musculu | pseu   | Q96s37 homo sapien | 088446 rattus norv | Q99jf0 mus musculu | Q9y694 homo sapien |        | Q96tcl homo sapien | homo   | OMO    | Q9r1q4 mus musculu | O08966 mus musculu | Q961j5 drosophila | Q63314 rattus norv | 002713 sus scrofa | 070577 mus musculu | Q9vik2 drosophila | Q63089 rattus norv | 077504 oryctolagus | Q9r0w2 rattus norv | 015244 homo sapien | P97558 rattus norv | Q96kh7 homo sapien | P70485 rattus norv | homo   | 2 mus  | homo   | 075751 homo sapien |

## ALIGNMENTS

| Qy                                                                   | Фр                                                                       | Qу<br>Дъ                                                                | Db Db                                                                 | ==0                                                                                                                                                               | DR SQ                                                                                                                                       | R R R                                     | 2000x                                                                                                                                                                             | DT DT                                                                                                                                                                                                                                                                    | RES<br>D                                     |
|----------------------------------------------------------------------|--------------------------------------------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------|
| 181 TGFSFLQIFSKNFEMFVVLFVLVGMGQISNYVAAFVLGTEILGKSVRIIFSTLGVCIFYA 240 | 121 QDVYLSTIVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRKNVLFVTMGMQ 180<br> | 61 AWRNHTVPLRLRDGREVPHSCRRYRLATIANFSALGLEPGRDVDLGQLEQESCLDGWEFS 120<br> | 1 MRDYDEVTAFLGEWGPFQRLIFFLLSASIIPNGFTGLSSVFLIATPEHRCRVPDAANLSS 60<br> | Query Match 99.8%; Score 2876; DB 4; Length 557;<br>Best Local Similarity 99.8%; Pred. No. 3.2e-216;<br>Matches 556; Conservative 0; Mismatches 1; Indels 0; Gaps | Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.  EMBL; BC012325; AAH12325.1; -  SEQUENCE 557 AA; 62735 MW; 9C3E15059F20E6A4 CRC64; | SEQUENCE FROM N.A. TISSUE-LUNG CARCINOMA; | MEMBER 5.  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCHI_TaxID=9606; | 096EH6; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) SIMILAR TO SOLUTE CARRIER FAMILY 22 (ORGANIC CATION TRANSPORTER), | RESULT 1<br>Q96EH6 PRELIMINARY; PRT; 557 AA. |

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 MEDLINE-2056258; PubMed-11010964;
Tannai I., Ohashi R., Nezu J., Sai Y., Kobayashi D. Shimane M., Tsuji A.;
Molecular and Functional Characterization of Orgatiransporter Family in Mice.";
Transporter Family in Mice.";
J. Biol. Chem. 275:40064-40072(2000).
-i- SUMILARITY: BELONGS TO THE SUGAR TRANSPORTER E EMBL; AB018436; BAA78343.1;
-therpro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
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01-NOV-1999
01-NOV-1999
01-DEC-2001
 Transmembrane.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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 NCBI_TaxID=10090;
 SLC22A9 OR OCTN3
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 FGYMVLPLFAYFIRDWRMLLVALTMPGYLCVALWWFIPESPRWLISQGRFBEAEVIIRKA
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 Score 2295.5; DB 1
Pred. No. 6.1e-171;
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 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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 C37FDCA6395DAD01 CRC64;
 MEMBRANE PROTEIN (BY AR TRANSPORTER FAMILY.
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 Kobayashi D., Oku
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 DB 11;
 Organic Cation/Carnitine
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Q9H015
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Matches 425; Conserv
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01-MAR-2001
01-DEC-2001
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY
-:- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
EMBL; Y09881; CAA71007.1; -.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
 Transmembrane. SEQUENCE 551
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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 TRANSPORT
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 77.2%;
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 Score 2227; DB 4;
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7; Mismatches 69;
 Created)
 Craniata; Vertebrata; Catarrhini; Hominidae
 C827A99AA78C9443 CRC64;
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 Hominidae;
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Matches 423
 014546 PRELIMINARY;
014546;
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
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 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 cation transporter, OCTN1.";
FEBS Lett. 419:107-111(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
EMBL; AB007448; BAA23356.1; -.
 MEDLINE=98086199; PubMed=9426230; Tamai I., Yabuuchi H., Nezu J., S
 Tamai I., Yabuuchi H., Nezu J., Sai Y., Oku A., Shimane M., "Cloning and characterization of a novel human pH-dependent
 SEQUENCE FROM N.A.
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 241
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SEQUENCE 551 AA;
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 InterPro; IPR003662; sub_transporter
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Last sequence update)
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 "Structural and functional characteristics pattern of OCTN1, an organic cation transpoplacenta.";
 MEDLINE=20286310; PubMed=10825452; MEDLINE=20286310; PubMed=10825452; Mang W., Wang
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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 Biochim. Biophys. Acta 1466:315-327(2000)
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PROSITE; PS00216; SUGAR_TRANSPORT_1;
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01-MAY-1999
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 SEQUENCE FROM N. .. TISSUE-KIDNEY;
STRAIN-C57BL 6J; TISSUE-KIDNEY;
MEDLINE-20558258; PubMed-11010964;
Mezu J., Sai
 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
EMBL; ABO16257; BAA36626.1; -.
EMBL; BC010590; AAK10590.1; -.
 TISSUE-BREAST TUMOR;
Strausberg R.;
 Shimane M., Tsuji A.;
"Molecular and Functional Characterization
Transporter Family in Mice.";
 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
 SLC22A4 OR OCTN1
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C-2001 (TIEMBLYE1. 19, Last annotation update)
(SOLUTE CARRIER FAMILY (ORGANIC CATION TRANSPORTER),
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 (Mouse).
 275:40064-40072(2000)
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Rođentia;
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 Craniata; Vertebrata; I
Sciurognathi; Muridae;
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 O9VCA2 PRELIMINARY;
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O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-DEC-2001 (TrEMBLrel. 1
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MEDITING-2019000; FUNDMENT-ALLEY,
Adams M.D., Celnikker S.E., Holt R.A., Evans C.A., Godayne J.D.,
Adams M.D., Celnikker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch (C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
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NCBI_TaxID=7227;
 ORCT OR CG6331
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 SEQUENCE FROM N.A.
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 74.5%;
72.2%;
 553
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13,
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Pred. No. 1
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 Mismatches
 548
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1.9e-159;
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 Hexapoda;
 Brachycera;
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 Gaps
 120
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RT Science 287.2185-2195(2000).
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 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies S., de Pablos B., Delcher A., Deng Z., Mays A.D., Deu I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann
 Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
EMBL, AB003747; AAF56271.1; -.
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 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., W. C., Lewis S.E., Rubin G.M., Celniker S.;
 STRAIN=Y, CN BW SP;
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 FlyBase; FBgn0019952; Orct.
InterPro; IPR003662; sub_transporter
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Pred.
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 No. 6.
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5.3e-61;
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 Ferriera S., Fleischmann
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 Length
 Indels
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Smith H.O
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 MEDLINE-POUL STAILEY K., Shirras A.U.,
Taylor C.A.M., Stanley K., Shirras A.U.,
The Orct gene of Drosophila melanogaster codes
"The Orct gene of Drosophila melanogaster codes
 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
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 ORCT OR CG6331.
 001384;
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 cation transporter with six or 12 Gene 201:69-74(1997).
 SEQUENCE FROM N.A.
MEDLINE=98072431; PubMed=9409773;
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SEQUENCE 548
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FlyBase; FBgn0019952; Orct.
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 InterPro;
 516
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 DQMLRVKGMKHRKTPSHTRMLKDG
 GLGASSMVARVGGILAPYLKLLGEIWRPLPLIICGALSLTAGILSLLLPETLNKPMPETI
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 Conservative
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18, Last annotation updat
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Pred. No. 1.3e-60;
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 Gaps
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hrandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Bayland A., An H.-J., Andrews-Pfannkoch C.C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Botshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gentera S., Fleischmann W.,
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RA Melson D.R., Nelson K.A., Howland T.J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPhersson D.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
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CG13610 PROTEIN.
 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; H
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 Drosophila
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 534
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 Hexapoda; Insecta; a; Brachycera; Muscomorpha;
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Q95R48
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Best Local Similarity
Matches 183; Conserv
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 Eukaryota;
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 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

science 287:2185-2195(2000).

1. SUBCELULIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARIT INTEGRAL MEMBRANE PROTEIN (BY SIMILARIT SMILLARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 Transmembrane
 InterPro; IPR003662; sub_transporter
Pfam; PF00083; sugar_tr; 1.
 -!- SIMILARITY: BELONGS TO THE EMBL; AE003747; AAF56270.1; -. FlyBase; FBg00039176; CG13610.
 520
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melanogaster (Fruit fly)
Metazoa; Arthropoda; Tra
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 PRELIMINARY;
 Conservative
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 63166 MW;
 28.3%;
 19,
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Last annotation updat
 Score
Pred.
 PRT;
 0D9B979469395E60 CRC64;
Tracheata; Hexapoda;
 Mismatches
 542
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No. 1
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 DB 5;
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 212;
 Length
 Indels
Insecta;
 SIMILARITY).
 52;
 Gaps
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ID Q9
AC Q9
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Matches 184; Conser
O96RUO PRELIMINARY; PRT; 577 AA.
O96RUO;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence upda
O1-DEC-2001 (TrEMBLrel. 19, Last annotation upo
GORGANIC CATION TRANSPORTER OKB1.
HOMO Sapiens (Human).
BUKaryota; Metazoa; Chordata; Craniata; Verteb:
Mammalia; Eutheria; Primates; Catarrhini; Homis
NCBL_TaxID=9606;
 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Mirada A., Mungall C., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (CCT-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AY061615; AAL291631; -
SEQUENCE 567 AA; 63254 MW; 3B10F3D8E19A0225 CRC64:
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 28.1%; 32.2%;
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 Craniata; Vertebrata; Catarrhini; Hominidae
 Mismatches
 542
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 DB 5; L
3.9e-55;
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 Hominidae;
 update)
 Brachycera;
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 Indels
 Euteleostomi;
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Best Local
 Matches 188;
 SEQUENCE FROM N.A.
Okabe M., Abe T.;
"Molecular identification of OKBl.";
 Submitted (MAY-2000) to the EMBL/GenBank/DDBJ EMBL; AF268892; AAK58593.1; -. SEQUENCE 577 AA; 64584 MW; ClDODF07C60488
 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel 19, ORGANIC CATION TRANSPORTER CCT-1 OR F52F12.1B.
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MEDLINE-99227113; PubMed=10209228;
Wu X., Fei Y.J., Huang W., Chancy of the F52F12.1 gene pro-
 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
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 HNHSNWSLEDTGALLSSGOKDYYTVQLQNGEIWELSRCSRNKR----ENTSSLGYE----
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 RDYDEVTAFLGEWGPFQRLIFFLLSASIIPNGFTGLSSVFLIATPEHRCRVP-----
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Caenorhabditis elegans.
 Biochim. Bioph [2]
SEQUENCE FROM
 investigating biology.", Science 282:2012-2018 (1998). Science 282:2012-2018 (1998). "INTEGRAL MEMBRANE PROTEIN (BY -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. EMBL; AF110415; AAF21932.1; -. EMBL; 283228; CAC70093.1; -.
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AMALLGVVAMFIRRWRQLTFFCNAPFAFYIIYYFFLPESPRWSVSVGKWADAKKQLKKIA 295
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GH27944P.
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-!- SIMILARITY: BELONGS TO THE SUGAR

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Pfam, PF00083; sugar_tr; 1.
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Science 282:2012-2018(1998)
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 Genome sequence of the nematode C.elegans: A platform
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 244 AMALLGVVAMFIRRWRQLTFFCNAPFAFYIIYYFFLPESPRWSVSVGKWADAKKQLKKIA
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 DVYLSTIVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGQLSDRFGRKNVLFVTMGMQT 181
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CG4630.
 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J. Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY058475; AAL13704.1; -. SEQUENCE 563 AA; 62138 MW; D3E2CB4096A195CB CRC64;
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Drosophila melanogaster (Fruit fly).
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Drosophila melanogaster
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RA Spler E., Spradling A.C., Stapleton M., Skrong R., Sinth T.,
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RA Cheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,
RT McHoerone Sequence of Drosonchila melanogaster ".
 Matches
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandr Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.
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 "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann
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 Total number of hits satisfying chosen parameters:
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 Perfect score:
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2: qb_htq

3: qb_in:

4: qb_om

5: qb_p?

7: qb_p?

7: qb_p?

9: qb_f

10: qf

11: q}

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## ALIGNMENTS

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OCTN2. high Direct Submission Submitted (28-MAY-1998) Jun-ichi Nezu, Chugai Research Institute Submitted (28-MAY-1998) Jun-ichi Nezu, Chugai Research Institute for Molecular Medicine, Inc., Gene Search Program; 153-2 Nagai, Niihari, Ibaraki 300-4101, Japan (E-mail:nezuj@cimmed.com, Tel:81-298-30-6211, Fax:81-298-30-6270) 2 (sites) Tamail., Ohashi,R., Nezu,J., Yabuuchi,H., Oku,A., Shimane,M., Sai,Y. and Tsuji,A. Molecular and functional identification of sodium ion-dependen Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Nezu, J. Homo sapiens Kidney cDNA to mRNA. (bases 1 to 1831) cular and functional identification of sodium ion-dependent, affinity human carnitine transporter OCTN2 ďď complete cds. mRNA linear PRI 06-FEB-1999

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 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvanch Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
 BC Cancer Agency, Vancouver, BC, info@bcgsc.bc.ca
 Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Con
DNA Sequencing by: Genome Sequence Centre,
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Schomig, E., Spitzenberger, F.,
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Submitted (07-OCT-1997) D. Department of Pharmacology,
 Molecular cloning and characterization proteins from rat kidney FEBS Lett. 425 (1), 79-86 (1998)
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 and Grundemann, D.
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|            | IIII<br>AGAGA 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Ъ                    |
| -          | 828 gtgcatattttatgcatttggctacatggtgctgccactgtttgcttacttcatccgaga 887                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Qy                   |
|            | ω i                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                      |
|            | 58 tatrottananananaaattottananaaattoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatoottatootta |                      |
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|            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                      |
|            | 7 (                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Qy                   |
|            | 588 999ctccttcatttca999ca9ct9tca9aca99ttt9gccg9aagaatgtgctgttcgt 647 51                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | D 04                 |
|            | 91 GTGTAAGGATGACTGGAAAGCCCCCACTCACCACCTCTTTTTTCGTGGGTGTGCTGAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                      |
|            | 28 qtqtqaqqacqactqqaaqqccccactcacaattcccttqttcttcttcttcattqataataataataataataataataataataataata                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                      |
|            | 468 tygotyggagttcagtcaggacgtctacctgtccaccattgtgaccgagtggaacctggt 527                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Ş 8                  |
|            | 371 GGGCTGCAGCCGGGACGGGACCTGGAGCAGCTAGAGCAAGAGAACTGCCTGGA 430                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                      |
|            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | OV                   |
|            | 348 99499tgcccaaagttgccgcgctaccggctsgccaacttgccaacttctcggcgct 407                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Db                   |
| ·          | CGTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                      |
|            | 288 cgcgaacctgagcagcgcctggcgcaaccaactgtcccactgcggctgcggacggccg 347                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Qy                   |
|            | 228 cggcctgtcctccgtgttcctgatagcgaccccggagcacccgctgccgggtgccggacgc 287                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Db Qy                |
|            | سا                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Db .                 |
| <b>818</b> | <u>.</u>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Qy                   |
|            | 108 ggcctctgagggcggcatgcgggactacgacgaggtgaccgccttcctgggcgagtgggg 167<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | B 8                  |
|            | 11 GCCCCTCAGCCCCCCCTCTCCCCGCTCTCCGGGTATCCCCCGGACGGGTGTTGTG 70                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Db                   |
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|            | GOLSDREGARNULEIJENGKYNDYRAPITTSLEFYGYLMGSFIS GOLSDREGARNULEIJENGMOTGESFLÖLESVNEMETVLEVLYGMGQISNYVAMFYLG TEILSKSIRIIFATLGVCIFYARGFMVLDLFAYEIRDMRMLLLALTVDGVLCGALWWF LPESPRWLISQGRVKEAEVIIRKAAKFNGIVAPSTIFDPSELQDLNSKKPQSHHIYDL VRTRNIRIITIMSIILWLTISVOYFGLSLDTPMLHGDIYVNCFLLAAVEVPAYVLAWL LUQHLPRRYSISAALFLGGSVLLFIQLVPSELFYLSTALVMVGKFGITSAYSMYVYYT AELYPTVRNMGYGVSSTASRLGSILSPYFVYLGAYDRFLPYLLMGSLTILTIAILTLF FPESFGAPLPDTIDQMLRVKGIKQWQIQSQTRTQKDGGESPTVLKSTAF" 681 a 786 c 747 g 793 t                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | BASE (ORIGI)         |
| _          | TPEHRCLVPHTVNLSSAWRNHSIPLETKDGRQVPQSCRRYRLATIANFSALGLEPGRD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                      |

| RESULT 5 AF110416 LOCUS DEFINITION ACCESSION VERSION KEYWORDS                                                                              | Qy 1788 a<br>  Db 1751 A                              | Db 1691 C                                                             | 1631                   | 1608<br>1571                  | Qy 1548 o                                                             | 488                                                   | 1428<br>1391                                                          | Qy 1368 d                                                             | Qy 1308 Db 1271                                                       | 1248<br>1211                                                                        | Qy 1188<br>Db 1151                                                    | Qy 1128<br>Db 1091                                                 | 1068                                                                  | 71                                                    | Qy 948<br>Db 911                                                      | 888<br>851                                                            |
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|                                                                                                                                            |                                                       |                                                                       |                        |                               |                                                                       |                                                       |                                                                       |                                                                       |                                                                       |                                                                                     |                                                                       |                                                                    |                                                                       |                                                       |                                                                       |                                                                       |

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Nu,X., Huang,W., Prasad,P.D., Seth,P.,
Chen,J., Conway,S.J. and Ganapathy,V.
Functional characteristics and tissue corganic cation transporter 2 (OCTN2), a
 Wu,X., Huang,W., Prasad,P.D.,
Conway,S.J. and Ganapathy,V.
Direct Submission
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Sekine,T., Kusuhara, F.
Kanai,Y. and Endou, H.
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Submitted (26-AUG-1998) Takashi Sekine, Kyorin University, School of Medicine, Department of Pharmacology and Toxicology; 6-20-2 Shinkawa, Mitaka, Tokyo 181, Japan (E-mail:QZV07422@nifty.ne.jp, Tel:0422-47-5511(ex.3451), Fax:0422-79-1321)
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A missense mutation of mouse OCTN2, a sodium-dependent cotransporter, in the juvenile visceral steatosis mouse
Biochem, Biophys. Res. Commun. 252 (3), 590-594 (1998)
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 Submitted (24-JUN-1998) Jun-ichi Nezu, Chugai Research Institute for Wolecular Medicine, Inc., Gene Search Program; 153-2 Nagai, Nithari, Ibaraki 300-4101, Japan (E-mail:nezuj@cimmed.com, Tel:81-298-30-6211, Fax:81-298-30-6270)

Location/Qualifiers
 Nezu, J., Tamai, I., Oku, A., Ohashi, R., Yabuuchi, H., Hashimoto, N., Nikaido, H., Sai, Y., Koizumi, A., Shoji, Y., Takada, G., Matsulshi, T., Yashino, M., Kato, H., Ohura, T., Tsujimoto, G., Hayakawa, J., Shimane, M. and Tsuji, A.

Shimane, M. and Tsuji, A.

Primary systemic carnitine deficiency is caused by mutations in a gene encoding sodium ion-dependent carnitine transporter nat. Genet. 21 (1), 91-94 (1999)
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Wu,X., Huang,W., Prasad,P.D., Rajan,D.
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 Direct Submission

Direct Submission

Submitted (07-OCT-1998) Jun-ichi Nezu, Chugai Research Institute for Molecular Medicine, Inc., Gene Search Program: 153-2 Nagai, Nihari, Ibaraki 300-4101, Japan (E-mail:nezuj@cimmed.com, Tel:81-298-30-6270)

Tel:81-298-30-6270,

Location/Qualifiers
 Tamai, I., Ohashi, R., Nezu, Jl., Sal, I., Nowal Shimane, M. and Tsuji, A.
Molecular and Functional Characterization of Cation/Carnitine Transporter Family in Mice J. Biol. Chem. 275 (51), 40064-40072 (2000)
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 Submitted (18-SEP-1997) Jun-ichi Nezu, Chugai Research Ins
for Molecular Medicine, Inc., Gene Search Program; 153-2 Niihari, Ibaraki 300-4101, Japan (E-mail:nezu)@cimmed.com
 reaction transporter, FEBS Lett. 419 (1),
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|     | 544          | 4-                                                                 | Db       |

| ,                                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                            |                                                             |
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| gth 2258;<br>ls                                                                                                                                                                                                        | Match 53.2%; Score 973.2; DB 10; Length ocal Similarity 74.2%; Pred. No. 3.1e-167; Pred. No. 3.1e-167; Mismatches 428; Indels                                                                                                                                              | Query Match<br>Best Local<br>Matches 12                     |
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|                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                            | gene<br>CDS                                                 |
| Street, Augusta, GA                                                                                                                                                                                                    | 2 (bases 1 to 2258) Wu,X., Wang,H., Leibach,F.H. and Ganapathy,V. Direct Submission Submitted (17-JUL-1999) Department of Biochemi Biology, Medical College of Georgia, 1120 15th 30912-2100, USA Location/Qualifiers                                                      | REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUTCE             |
| Conwayc,S.J., ind tissue distribution insporter, cloned from (2000)                                                                                                                                                    | 1 (bases 1 to 2258) Wua, X., Georgeb, R. L., Huanga, W., Wanga, H., Cor<br>Leibacha, F. H. and Ganapathya, V. Structural and functional characteristics and<br>pattern of rat OCTN1, an organic cation transplacenta Biochim. Biophys. Acta 1466 (1-2), 315-327 (20286310) | REFERENCE AUTHORS TITLE JOURNAL MEDLINE                     |
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 Tamai,I., Ohashi,R., Nezu,Ji., Sai,I., Shimane,M. and Tsuji,A.
Shimane,M. and Tsuji,A.
Molecular and Functional Characterization of Cation/Carnitine Transporter Family in Mice Cation/Carnitine Transporter Family in Mice II. Biol. Chem. 275 (51), 40064-40072 (2000)
 Submitted (15-JUL-1998) Jun-ichi Nezu, Chugai Research Institute for Molecular Medicine, Inc., Gene Search Program; 153-2 Nagai, Niihari, Ibaraki 300-4101, Japan (E-mail:nezuj@cimmed.com, Tel:81-298-30-6211, Fax:81-298-30-6270)
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linear ic cation

ROD 12-JUL-2001
transporter),

BC010590

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 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hump
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 Email: cgapbs-r@mail.nih.gov
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useful in de abnormality homologous with organic cation transporters OCT1 and OCT2, I in design of new drugs for treatment of diseases due to mality of the transporter functions

Claim <u>ب</u> Page 56-61; 97pp; Japanese.

The present sequence encodes a protein with cation transporting activity. The genes are significantly homologous with organic cation transporters OCT1 and OCT2. The genes may used in drug development, particularly in the treatment of diseases due to abnormality of the organic cation transporter functions e.g. fatty liver, heart diseases and cancers, by controlling such as by inhibition or activation. Administration of anti-tumour and anticancer drugs in combination with a transporter protein inhibiting agent allows the agents to penetrate into the diseased cells to enhance the drug action.

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 This sequence represents the cDNA encoding the human carnitine transporter protein OCTN2. The sequence can be used as a target for diagnosis of systemic carnitine deficiency by detecting the presence of mutations in the sequence, especially seen in the disease juvenile visceral steatosis (jvs). The wild type OCTN2 gene can be used in th gene therapy of the disease state.
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 OCTN2; diagnosis; juvenile visceral
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 16-MAR-2000
 WO200014210-A1
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AC AAS67216;
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 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC considerable are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical climating of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS6419-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed on the printed of the printed o
 Query Match
Best Local
 Matches 1831;
 2683
 2743
 2803
 2863
 3043
 2923
 2983
 3103
 3163
 541
 481
 Sequence 3261 BP; 878
 421
 361
 301
 241
 181
 121
 61
 ftp.wipo.int/pub/published_pct_sequences
ctcatcttcttcctgctcagcgccagcatcatccccaatggcttcaccgggcctgtcctcc
 999c9c9acgt99acct999gcagct9gagcaggagagct9tct9gat9gctgggagttc
 agctgccgccgctaccggctcgccaccatcgccaacttctcggcgctcgggctggagccg
 agcgcctggcgcaaccacactgtcccactgcggctgcgggacggccgcgaggtgccccac
 9tgttcctgatagcgaccccggagcaccgctgccgggtgccggacgcccgcgcaacctgagc 300
 cacgcgcaaagcccgccgcgttcccagaccccaggccgcgctctgtgggcctctgagggc 120
 GGGCGCGACGTGGACCTGGGGCAGCTGGAGCAGGAGCTGTCTGGATGGCTGGGAGTTC
 GTGTTCCTGATAGCGACCCCGGAGCACCGCTGCCGGGTGCCGGACGC¢GCGAACCTGAGC
 ggcatgcgggactacgacgaggtgaccgccttcctgggcgagtggggggccttccagcgc
 AGCTGCCGCCGCTACCGGCTCGCCACCATCGCCAACTTCTCGGCGCGCT¢GGGCTGGAGCCG
 AGCGCCTGGCGCAACCACACTGTCCCACTGCGGCTGCGGGACGGCCG¢GAGGTGCCCCAC
 GGCATGCGGGACTACGACGAGGTGACCGCCTTCCTGGGCGAGTGGGGGGCCCTTCCAGCGC
 CACGCGCAAAGCCCGCCGCGTTCCCAGACCCCAGGCCGCGCTCTGTGGGCCTCTGAGGGC
 Similarity
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 Score
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 839
 Mismatches
 1831;
No. 0;
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 other;
 Indels
 Length
 3261;
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 Gaps
 2624
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 2804
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 2984
 180
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 ATCCGGATGGTCACCATGTCCATAATGCTGTGGATGACCATATCAGTGGGCTATTTT
 GACCTAAGTTCCAAGAAGCAGCAGTCCCACAACATTCTGGATCTGCTTCGAACCTGGAAT
 TCCCCCCGATGGCTCATCTCTCAGGGACGATTTGAAGAGGCAGAGGTGATCATCCGCAAG
 GCATTTGGCTACATGGTGCTGCCACTGTTTGCTTACTTCATCCGAGACTGGCGGATGCTG
 GAAATTCTTGGCAAGTCAGTTCGTATAATATTCTCTACGTTAGGAGTGTGCATATTTTAT
 TTTGTCCTTGTAGGCATGGGCCAGATCTCCAACTATGTGGCAGCATTTGTCCTGGGGACA
 TTCGTTTACCTTGGTGCCTACGACCGCTTCCTGCCCTACATTCTCATGGGAAGTCTGACC
 AACATGGGTGTGGGAGTCAGCTCCACAGCATCCCGCCTGGGCAGCATCCTGTCTCCCTAC
 {	t ATCCTGACAGCCATCCTCACCTTGTTTCTCCCAGAGAGCTTCGGTACCCCACTCCCAGAC
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RESULT AAX26902
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XX OTGG
KW OTGG
KW Hear
XX MUSE
FH CDS
FF CDS
FF CDS
FF COS
FF 07-2
XX W095
XX W095
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XX CO
 Qy
 Db
 밁
 Ωy
 Дb
 Qγ
 DЪ
 Query Match
Best Local Similarity
Matches 1505; Conserv
 The present sequence encodes a protein with cation transporting activity. The genes are significantly homologous with organic cation transporters OCT1 and OCT2. The genes may used in drug development, particularly in the treatment of diseases due to abnormality of the organic cation transporter functions e.g. fatty liver, heart diseases and cancers, by controlling such as by inhibition or activation. Administration of anti-tumour and anticancer drugs in combination with a transporter protein inhibiting agent allows the agents to penetrate into the diseased cells to enhance the drug action.
 1363
 1801
 1423
 Nezu
 AAX26902;
 AAX26902
 Claim
 useful in design abnormality of the
 Genes
 20-MAY-1998;
08-SEP-1997;
 07-SEP-1998;
 Organic
 Sequence
 P-PSDB;
 18-MAR-1999
 WO9913072-A1
 23-JUN-1999
 (CHUG-)
 heart
 133
 69
 73
 9
 4
 musculus
 encoding a
 1999-215062/18.
DB; AAY01652.
 ccgccgcgttcccagaccccaggccgcgctctgtgggcctctgagggcggcatgcgggac 132
tacgacgaggtgaccgccttcctaggcgagtgggggcccttccagcgcctcatcttcttc
 tacgacgaggtgaccgccttcctgggcgagtgggggcccttccagcgccctcatcttcttc 192
 ccacggtgtccccttattcccatacgggcgctgtgggaggctgaggacggcatgcgggac
 ic cation disease;
 AGGATGTTAAAAAGATGGTCAAGAAAAGGCCCCACAATCCTTAAAAAGCACAGCCTTCTAACAT 1364
 homologous with organic cation transporters OCT1 and I in design of new drugs for treatment of diseases due mality of the transporter functions
 <u>ب</u>
 CHUGAI
 1888
 standard;
 Page
 73.9
hilarity 85.6
Conservative
 (first
 B₽;
 80-85;
 RES
 transporter; OCT1; (
cancer; anti-tumour
 98JP-0156660.
97JP-0260972.
 98WO-JP04009
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 Location/Qualifiers 60..1733
 392
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 DNA;
 entry)
 97pp;
 A;
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 1888
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 cation
 Score 1352.6;
Pred. No. 0;
0; Mismatches
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 OCT2;
 MEDICINE
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 1352.
No. 0
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 188
 809
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 368
 308
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RESULT
AAAO9890
ID AAAC
XX AAA
AC AAAC
XX Mous
XX Orga
VX Orga
VX Orga
VX Out
VX Juve
VX Mus
XX Juve
VX Mus
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PD 16-M
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 밁
 Organic
OCTN2; d
Systemic carnitine cation transporter,
 1749
 1449
 1513
 1389
 WPI; 2000-256966/22.
P-PSDB; AAY83930.
 OCTN2; diagnosis; systemic ca
juvenile visceral steatosis;
 1689
 1693
 1569
 1509
 1573
 07-SEP-1998;
 07-SEP-1999;
 16-MAR-2000
 WO200014210-A1
 Mus
 Mouse
 05-JUL-2000
 AAA09890
 musculus.
 gcaaaaaactgattggaaa
 gggagaaactgaagaggaa
 gatggtcaagaaaggcccacaatccttaaaagcacagccttctaacatcgcttccagtaa
 atgctaagggtcaaaggaataaaacagtggcaaatccaaagccagacaagaatgcaaaaa
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 gccactgccctcttcctgggtggcagtgtccttctcttcatgcagctggtacccccagac
 gatggtgaagaaagcccaacagtcctaaagagcacagccttctaaca¢cctgtccagaag
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 teggetgeeetttteetgggtggeagtgteettetetteatgeaget@gtgeetteagaa
 OCTN2
 cation
 CHUGAI
 standard;
 CDNA
 (first
 RES
 98JP-0252683
 transportation; mouse;
 99WO-JP04853
 sequence
 deficiency, useful as
 INST
 CDNA; 1888
 MOLECULAR
 1831
 carnitine
 SS
gene OCTN2
diagnostic
 MEDICINE
 deficiency;
 carnitine
 encoding
 transporter; mutation; q
 part
 of
 gene
 protein;
 therapy;
 1268
 1688
 1628
 1692
 1568
 1632
 1508
 1572
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04 DP OA DP
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60
60
 γQ
 P 04
 Дb
 Qy Db Qy
 SXCCCCCXXX
 Query Ma
Best Loc
Matches
 This sequence transporter procan be used as by detecting the in the disease gene can be used.
 Sequence
 Example
 673
 669
 609
 549
 613
 489
 553
 429
 493
 369
 433
 249
 313
 253
 789
 793
 733
 309
 189
 129
 193
 729
 Local Similarity 85.0 tes 1505; Conservative
 69
 is sequence represents the cDNA encoding the mouse carnitine ansporter protein OCTN2. The corresponding human sequence (AAA09889) in be used as a target for diagnosis of systemic carnitine deficiency detecting the presence of mutations in the sequence, especially seer the disease juvenile visceral steatosis (jvs). The wild type OCTN2 ne can be used in the gene therapy of the disease state.
 9
 ctgctcagcgccagcatcatccccaatggcttcaccggcctgtcctccgtgttcctgata
 tacgacgaggtgaccgccttcctgggcgagtgggggcccttccagcgccctcatcttcttc
 ccgccgcgttcccagaccccaggccgcgctctgtgggcctctgagggcggcatgcgggac
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(first

entry)

ΒP

Mouse

OCTN3

NO:2.

592

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Best Local Similarity
Matches 1363; Conserv
 The present invention describes a mouse organic cation transporter protein (CCTN3). Also described are: (1) a method for screening compounds for their ability to regulate the transport of an organic cation into the cell, by generating a cell expressing CCTN3 at the cell membrane, contacting with the compound and organic cation, and observing the degree of transport of the organic cation; and (2) a method for screening compounds for their ability to be transported in the cell by OCTN3, by generating a cell expressing OCTN3 at the cell membrane, contacting with the compound and observing the degree of transport of the compound. OCTN3 can be used for the identification of regulators of the transport of organic cations (especially carnitine) into cells by OCTN3, for use as drugs. The present sequence encodes
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The present sequence encodes a protein with cation transporting activity. The genes are significantly homologous with organic cation transporters OCT1 and OCT2. The genes may used in drug development, particularly in the treatment of diseases due to abnormality of the organic cation transporter functions e.g. fatty liver, heart diseases and cancers, by controlling such as by inhibition or activation. Administration of anti-tumour and anticancer drugs in combination with a transporter protein inhibiting agent allows the agents to penetrate into the diseased cells to enhance the drug action.
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Sequence

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 The present sequence encodes a protein with cation transporting activity. The genes are significantly homologous with organic cation transporters OCT1 and OCT2. The genes may used in drug development, particularly in the treatment of diseases due to abnormality of the organic cation transporter functions e.g. fatty liver, heart diseases and cancers, by controlling such as by inhibition or activation. Administration of anti-tumour and anticancer drugs in combination with a transporter protein inhibiting agent allows the agents to penetrate into the diseased cells to enhance the drug action.
 Genes homologous with organic cation transporters OCT1 auseful in design of new drugs for treatment of diseases abnormality of the transporter functions
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 tgtaggcatgggccagatctccaactatgtggcagcatttgtcctggggacagaaattct
 attcagcttcgtgcagattttctcaaccaactgggagatgttcactgtgttgtttgccat
aaaagatggtc
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 ccttggtgcctacgaccgcttcctgccctacattctcatgggaagtctgaccatcctgac
 tytygyaytcayctccacaycatcccycctygycaycatcctytctccctacttcyttta
 cttctccatgttgtatgtcttcactgcggagctctacccaaccctggtcaggaacatggc
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 tatagctggggtgctattctggggaggaggtgtgcttctcttgatccaagtggtacctga
 gcagatgcagaaagtgagagggttcagatgtgggaaaaaaatcaacagtctcagtggacag
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 agccatcctcaccttgtttctcccagagagcttcggtaccccactcccagacaccattga
 cctgggcgcctataacagactcctaccctacatcctcatgggcagtctgactgtcctcat
 tgtgggcatcacctccatggcctctcgggtgggcagcatcattgccccctatttcgttta
 <u>agattataactttgtgtccattggactggtgatgctggggaaatttggggatcacctctgc</u>
 tgaagttccagcttacttcacagcctggctgctactgcgaaccctgccacggagatatat
 tctcaatgttcctaatttacatggagatgtctacctgaactgcttcctctctggcctgat
 tggaatcatcacgctttttttccctgaaagtttttggagtgactctaccagagaacttgga
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 1328
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 1146
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RESULT 9
AAH92241/c
ID AAH922
XX AAH922
XX AAH922
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XX BAC AAH922
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 the presence of genetic polymorphisms associated with inflammatory disease and correlating their occurrence with disease states. They used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a containing a polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and the containing and polymorphic site described in the exemplification of the containing and polymorphic site described in the exemplification of the containing and th
 Testing for the bowel disease,
 The present invention describes a method for detecting the present polymorphisms associated with inflammatory bowel diseases such subcerative colitis and Crohn's disease. The methods can be used
 Human
 09-OCT-2001
 AAH92241
 AAH92241 standard;
 (WHED)
 WO200142511-A2
 chromosome 5q31-33;
 Sequence
 10-DEC-1999; 99US-0170257
10-APR-2000; 2000US-0196046
 11-DEC-2000;
 14-JUN-2001
 invention.
 653
241
 533
 121
 593
 181
 61
 cacgcgcaaagcccgccgcgttcccagaccccaggccgcgctctgtggggcctctgagggc 120
 ctcatcttcttcctgctcagcgccagcatcatccccaatggcttcaccgggcctgtcctcc
 ggcatgcgggactacgacgaggtgaccgccttcctgggcgagtgggggcccttccagcgc 180
 CACGCGCAAAGCCCGCCGTTCCCAGACCCCAGGCCGCGCTCTGTGGGCCTCTGAGGGC
 516;
 inflammatory
 inflammatory bowel disease; Crohn's disease; ulcerative colitis; nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
 h 28.2%;
Similarity 100.0%;
16; Conservative
 for the presence of polymorphisms associated isease, using a hybridization assay -
 WHITEHEAD INST BIOMEDICAL ELLIPSIS BIOTHERAPEUTICS
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 Hudson TJ,
 Page
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 2000WO-US33632
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 DNA;
 bowel
 forensic
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 Lander ES,
 463pp;
 232
 disease related
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 Score 516; DB Pred. No. 1.4 0; Mismatches
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RESULT 1
AAAO9888
ID AAAO9888
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XX AAAO
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XX Orga
KW Orga
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 Query Match
Best Local S
Matches 516
 This sequence represents the genomic DNA encoding the human carnitine transporter protein CCTN2 (AAY83929). The complete genomic sequence contains 9 introns dispersed throughout the gene. The gene can be used as a target for diagnosis of systemic carnitine deficiency by detecting the presence of mutations in the sequence, especially seen in the disease juvenile visceral steatosis (jvs). The wild type OCTN2 gene ca
 Systemic carnitine cation transporter,
 Claim 1; Page 60-93;
 WPI;
 Nezu
 Sequence
 07-SEP-1999;
 Organic cation transportation; human; OCTN2; diagnosis; systemic carnitine
 (CHUG-) CHUGAI
 07-SEP-1998;
 16-MAR-2000
 WO200014210-A1
 Homo
 OCTN2; diagnosis;
juvenile visceral
 Human genomic OCTN2
 05-JUL-2000
 ,88860AAA
 AAA09888 standard; DNA;
 Local Si
hes 516;
 173
 481
 233
 421
 293
 361
 301
 413
 99
 353
 10
 sapiens
2000-256966/22.
 agtcaggacgtctacctgtccaccattgtgaccgag
 agctgccgccgctaccggctcgccaccatcgccaacttctcggcgctcgggctggagccg
 gggcgcgacgtggacctggggcagctggagcaggagctgtctggatggctgggagttc
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 GGGCGCGACGTGGACCTGGGGCAGCTGGAGCAGGAGAGCTGTCTGGATGGCTGGGAGTTC
 AGCTGCCGCCTACCGGCTCGCCACCATCGCCAACTTCTCGGCGCTCGGGCTGGAGCCG
 AGCGCCTGGCGCAACCACACTGTCCCACTGCGGGCTGCGGGACGGCCGCGAGGTGCCCCAC
 Similarity 100
16; Conservative
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 carnitine deficiency ransporter, useful as
 25871 BP;
 the
 (first
 gene
 RES INST MOLECULAR MEDICINE
 99WO-JP04853
 שיים בייטיינים (carnitine transporter protein; systemic carnitine deficiency; mutation; gene therapy; steatosis; ds.
 6356 A;
 therapy
 sequence
 entry)
 106pp;
 28.2%;
100.0%;
 25871
 6094 C;
 of the disease state.
 Japanese
 Score 5
 0;
 gene OCTN2
diagnostic
 ВP
 red. No. 5.1 Mismatches
 6408
 G;
 5.1e-112;
 encoding
tool -
 DB
 138
 516
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 Length 25871;
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Disclosure; Page
 Testing for the presence of bowel disease, using a hybri
 (WHED)
 Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
 AAH92757 standard;
 10-DEC-1999;
10-APR-2000;
 11-DEC-2000;
 14-JUN-2001
 WO200142511-A2
 Human inflammatory
 09-OCT-2001
 AAH92757;
 579
 481
 519
 421
 459
 339
 181
 361
 399
 301
 241
 279
 219
 121
 159
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 2001-367874/38
 sapiens
 999c9c9acgtggacctg9g9cagctggagcaggagctgtctggatggctgggagttc 480
 ctcatcttcttcctgctcagcgccagcatcatccccaatggcttcaccgggcctgtcctcc
 gggcgcgacgtggacctggggcagctggagcaggagagctgtctggatggctgggagttc
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 ggcatgcgggactacgacgaggtgaccgccttcctgggcgagtgggggcccttccagcgc
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 cacgcgcaaagcccgccgcgttcccagaccccaggccgctctgtgggcctctgagggc
 cacgcgcaaagcccgccgcgttcccagaccccaggccgcgctctgtgggcctctgagggc
 WHITEHEAD INST BIOMEDICAL RES. ELLIPSIS BIOTHERAPEUTICS CORP.
 Hudson TJ,
 2000US-0196046
 2000WO-US33632
 (first
 9908-0170257
 305; 463pp; English.
 bowel disease related
 DNA;
 entry)
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 gene fragment
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 Siminovitch
 with
 IGR3082a
 inflammatory
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present invention

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method for

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RESULT 12
AAH92756/c
ID AAH927
XX
AAH927
XX
AC AAH927
XX
BC Human
DE Human
XX
Human;
KW Human;
KW chromo
XX
Chromo
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 Query Match 18.3
Best Local Similarity 92.4
Matches 352; Conservative
 ulcerative colitis and Crohn's disease. The methods can be used to the presence of genetic polymorphisms associated with inflammatory disease and correlating their occurrence with disease states. They used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a genetic analysis and present sequence of the containing a polymorphic site described in the exemplification of the sequence.
 (WHED)
 single
 09-OCT-2001
 Daly M,
 10-DEC-1999;
10-APR-2000;
 11-DEC-2000;
 14 -JUN-2001
 WO200142511-A2
 chromosome
 Human inflammatory bowel disease related gene fragment IGR3081a
 AAH92756;
 AAH92756
 Sequence
 462
 402
 141
 102
 342
 321
 162
 381
 201
 282
 261
 222
 81
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 sapiens
 tctggatggctgggagttcag
 GGACGCCGCGAACCTGAGCAGCGCCTGGCGCAACAACAGTGTCCCGCCTGCGGCTGCGGGA
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 tetgtgggcetetgagggcetgcgggactacgacgaggtgaccgcettcetgggcga
 CCTGGATGGCTGGGAGTTCAG
 ggacgccgcgaacctgagcagcgcctggcgcaaccacactgtcccactgcggctgcgga
 CTTCAATGGTATGTCAGTCGTGTTCCTGGCGGGGACCCCGGAGCACCGCTGTCGAGTGCC
 GTGGGGGCCCTTCCAGCGCCTCATCTTCCTTCCTGCTCAGCGCCAGCATCATCCCCCAATGG
 gtgggggcccttccagcgcctcatcttcttcctgctcagcgccagcatcatccccaatgg
 TTTCGGAGCGGCAGTGGGAAGCATGCGGGACTACGACGAGGTGATCGCCTTCCTGGGCGA
 inflammatory bowel disease; Crohn's disease; ulcerative colitis; nucleotide polymorphism; SNP; chromosome 19p13; paternity test; some 5q31-33; forensic test; gene therapy; ds.
 WHITEHEAD
ELLIPSIS F
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 standard;
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 99US-0170257.
2000US-0196046.
 2000WO-US33632
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 BIOTHERAPEUTICS (
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 Score 334.6; DB 22;
Pred. No. 1.4e-69;
0; Mismatches 29;
 239
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Rioux J,
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RESULT 13
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 The present invention describes a method for detecting the presence polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to the presence of genetic polymorphisms associated with inflammatory disease and correlating their occurrence with disease states. They used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a generation and polymorphic site described in the exemplification of the properties.
 (WHED)
 chromosome 5q31-33;
 single
 AAH92200 standard;
 11-DEC-2000;
 14-JUN-2001
 Homo
 Human inflammatory bowel disease related
 09-0CT-2001
 Testing for the prese
bowel disease, using
 WPI;
 10-DEC-1999;
10-APR-2000;
 Sequence
 invention.
 Disclosure; Page 305;
 520
 463
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 403
 640
 343
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 283
 Local
 Match
 ctggatggctgggagttcagtcaggacgtctacctgtccaccattgtgaccgag
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 gegetegggetggagecgggegegacettggggecaggetggageaggagagetgt 462
 gacgccgcgaacctgagcagcgcctggcgcaaccacactgtcccactgcggctgcgggac 342
 GCGCTCGGGCTGGAGCCGGGGGGGCACGTGGACCTGGGGCAGCAGGAGAGCTGC
 GGCCGCGAGGTGCCCACAGCTGCAGCCGCTACCGGCTCGCCACCATCGCCAACTTCTCG
 9900909a99tgccccacagctgccgccgctaccggctcgccaccatcgccaacttctcg 402
 GACGCCGCGAACCTGAGCAGCGCCTGGCGCGAACAACAGTGTCCCGCTGCGGCTGCGGGAC 641
 2001-367874/38
 226;
 nucleotide polymorphism; SNI
 inflammatory
 WHITEHEAD INST BIOMEDICAL ELLIPSIS BIOTHERAPEUTICS C
 Similarity
 700
 Hudson
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 99US-0170257
2000US-0196046
 2000WO-US33632
 BP;
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 IJ,
 presence of polymorphisms associated
using a hybridization assay -
 134
 DNA;
 organism; SNP; chromosome 19p13; paternit forensic test; gene therapy; ds.
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 Score 221.2;
Pred. No. 1e-4
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ARESULT 1
AABL10925
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XX BL10
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Matches 222
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 The present invention describes a method for detecting the presence polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to
 genes
 23-MAR-2000;
11-JUL-2000;
 23-MAR-2001;
 WO200171042-A2
 Drosophila
 pharmaceutical;
 Drosophila; developmental biology;
 Drosophila melanogaster expressed polynucleotide SEQ ID NO
 ABL10925
 ABL10925 standard; cDNA;
 1295
 Sequence 700
 invention
 used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a containing a polymorphic site described in the exemplification of
 the
 Disclosure;
 Testing for the presence of polymorphisms associated with bowel disease, using a hybridization assay -
 New isolated nucleic a
genes from Drosophila
 Venter
 (PEKE)
 27-SEP-2001
 26-MAR-2002
 P-PSDB; ABB66822
 Local Signature 222;
 144
 204
 264
 84
 14
 presence of genetic polymorphisms associated with inflammatory ase and correlating their occurrence with disease states. They
 acatctttgtgaactgcttcctttcagcgatggttgaagtcccagcatatgtgttggcct
 GGATGACCATATCAGTGGGCTATTTTGGGCTTTCGCTTGATACTCCTAACTTGCATGGGG
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 2001-656860/75
 ACATCTTTGTGAACTGCTTCCTTTCAGCGATGGTTGAAGTCCCAGCATATGTGTTGGCCT
 JС,
 Similarity 96.
 PΕ
 CORP NY
 melanogaster
 Page 147;
 Adams M,
 2000US-191637P
2000US-0614150
 BP;
 2001WO-US09231
 (first entry)
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 detection reagent for detecting for elucidating cell signalling
 Score 217.2; I
Pred. No. 9.1e
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 217.2; DB 2
No. 9.1e-42;
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 The invention relates to an invention relates to an invention relates to an invention genes from Drosophila. capable of detecting 1000 or more genes from Drosophila signalling useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of cell-cell interactions in higher eukaryotes for the development of cell-cell interactions in higher eukaryotes for the development of cell-cell interactions in higher eukaryotes for the development of cell-cell interactions in higher eukaryotes for the development of cell-cell interactions in higher eukaryotes for the development of cell-cell interactions in higher eukaryotes for the development of cells.
 1116
 insecticides, therapeutics and pharmaceutical drugs. [1] discloses genomic DNA sequences (ABL16176-ABL30511), essequences (ABL01840-ABL16175) and the encoded proteins
 1533
 1413
 1353
 1236
 1056
 The sequence data for this patent did not form specification, but was obtained in electronic
 sequences (ABL0184(
(ABB57737-ABB72072)
 Claim
 1010
 Sequence
 at ftp.wipo.int/pub/published_pct_sequences.
 interactions
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 invention relates to an isolated nucleic acid detection reagent able of detecting 1000 or more genes from Drosophila. The invention ful in developmental biology and in elucidating cell signalling and
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 New isolated nucleic agenes from Drosophila interactions -
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11-JUL-2000;
 Claim 1; SEQ ID NO 27254; 21pp +
 Venter
 WO200171042-A2
 Drosophila melanogaster.
 pharmaceutical;
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 (PEKE
 27-SEP-2001.
 Drosophila
 ABL10924;
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 23-MAR-2001; 2001WO-US09231
 26-MAR-2002
 ABL10924 standard;
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 invention
 2001-656860/75.
DB; ABB66821.
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 catcccgcctgggcagcatcctgtctccctacttcgtttaccttggtgcctacgaccgct
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 melanogaster expressed
 Adams M,
 developmental
 2000US-191637P
2000US-0614150
 (first entry)
 relates
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 4533
 PWD,
 detection reagent for detecting for elucidating cell signalling
 biology; cell signalling; insecticide;
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Best Local Sin
Matches 618;
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 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB72072).
 2413
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 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
 Sequence
 950
 890
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 tcattccggagtctgcccgttggctcttgatgaagggtcgcaaggatgaggcctttgtga
 gcatattttatgcatttggctacatggtgctgccactgtttgcttacttcatccgagact
 gctgggagttcagtcaggacgtctacctgtccaccattgtgaccgagtggaacctggtgt 529
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 Conservative
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49
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Pred. No. 5.3e
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 Gaps
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Search completed: July 17, 2002, 01:52:40 Job time: 18926 sec

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Result
No.
 Minimum
Maximum
 Database
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Total number of hits satisfying chosen parameters:
 Sequence:
 Title:
Perfect score:
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 OM nucleic
 Searched:
 Scoring table:
 on
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 Score
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 Description
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 GENERAL INFORMATION:
 TELEFAX: (202)408-440 INFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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 OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
NAME: O'CONNOY, Steven p
REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 240
 APPLICANT: Grundema
APPLICANT: Gorboule
TITLE OF INVENTION:
 SEQUENCE CHARACTERISTICS:
LENGTH: 1885 base pair
 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)408-4000
 TITLE OF INVENTION:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 APPLICANT:
 APPLICATION NUMBER: US/
FILING DATE: March 18,
 Local Similarity
nes 622; Conserv
 STRANDEDNESS:
 FILING DATE: N
 COUNTRY:
 STATE:
 ADDRESSEE:
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 3: Finnegan, Henderson, Farabow, Garrett 1300 I Street, N.W., Suite 700
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Grundeman, Dirk
Grundeman, Dirk
Gorboulev, Valentin
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 Sequence 108, Application US/08592126 Patent No. 5821091 GENERAL INFORMATION:
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Best Local Similarity
Matches 162; Conserv
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 109:
 APPLICANT: Gregory DO TITLE OF INVENTION: TITLE OF INVENTION: INVE
 STREET: 350 Campa
CITY: Palo Alto
STATE: CA
COUNTRY: USA
 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 CORRESPONDENCE ADDRESS:
 HYPOTHETICAL:
ANTI-SENSE: NO
 SEQUENCE CHARACTERISTICS:
LENGTH: 481 base pairs
 CURRENT APPLICATION DATA:
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 CORRESPONDENCE
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 MOLECULE TYPE:
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 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
 ADDRESSEE:
 TOPOLOGY:
 STRANDEDNESS:
 TYPE: nucleic acid
 REGISTRATION NUMBER:
 FILING DATE:
 APPLICATION NUMBER:
 ADDRESSEE:
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ZIP: 20005-3315
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MEDIUM TYPE: Floppy disk
 APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
TITLE OF INVENTION: Transport protein Which Effects The
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and or Pharmaceuticals,
TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
 NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
 CORRESPONDENCE ADDRESS:
 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 NUMBER OF SEQUENCES:
 ANTI-SENSE:
 MOLECULE TYPE:
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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 STREET:
 LENGTH: 370 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 COUNTRY:
 STREET: 350 Caml
 ADDRESSEE:
 FILING DATE:
 APPLICATION NUMBER:
 COUNTRY: U
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 Washington
 Similarity
 D.C
 CA
 E: Finnegan, Henderson, Farabow, Garrett & Dunner
1300 I Street, N.W., Suite 700
 350 Cambridge Avenue, Suite
 USA
 USA
 Conservative
 NO.
 NO
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 95.2%;
 G78.seq
 US/08/592,126
 108:
 4600-0111
 Score 155.2; DB 1
Pred. No. 1.8e-29;
0; Mismatches 8
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 DB 1;
 8
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 Indels
 0;
 Gaps
 102
 0;
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US-08-501-572-4
 Query Match
Best Local Similarity
Matches 566; Conserv
 REFERENCE/DOCKET NUMBER: 0248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 1025
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 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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 STRANDEDNESS:
TOPOLOGY: lin
 NAME: Toohey, Kimberlin M
REGISTRATION NUMBER: 35,391
 CLASSIFICATION: 424
 APPLICATION NUMBER:
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 02481.1453-00000
 Score 155; DB 3; Pred. No. 3.8e-29;
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 #1.30
 Length 1882;
 Indels
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 Gaps
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 Sequence 4, Application Patent No. 6063766
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
 APPLICANT:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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 TITLE OF INVENTION: Transport protein Which Effects The TITLE OF INVENTION: Transport Of Cationic Xenobiotics and\or Pharmaceuticals.

TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
 1519
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 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-BOSE #1.0,
CURRENT APPLICATION DATA:
 APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Gorboulev, Valentin
 1279
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 CORRESPONDENCE ADDRESS:
 1459
 1339
 TELEPHONE: (202)408-4000
 ATTORNEY/AGENT INFORMATION:
 NUMBER OF SEQUENCES:
 STATE: D
COUNTRY:
 STREET: 1300 I S
CITY: Washington
 CLASSIFICATION:
 APPLICATION NUMBER: FILING DATE: March
 REFERENCE/DOCKET NUMBER: 248
 NAME: O'Connor, Steven REGISTRATION NUMBER: 41
 TELEFAX:
 ADDRESSEE:
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 20005-3315
 CHARACTERISTICS:
 D.C
 E: Finnegan, Henderson, Farabow, Garrett & 1300 I Street, N.W., Suite 700
 USA
 (202)408-4400
 March 18,
 US/09040444
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TOPOLOGY: line
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47.4%;
 Score 155; DB 3; I
Pred. No. 3.8e-29;
0; Mismatches 615;
 Length 1882;
 Indels
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 Gaps
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 US-08-501-572-6
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Best Local :
 Sequence 6,
 Patent No.
 Matches
 TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1896 base pairs
 GENERAL
 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport protein Which Effects The
TITLE OF INVENTION: Transport Of Cationic Xenobiotics an
TITLE OF INVENTION: DNA Sequences Encoding It And Their
NUMBER OF SEQUENCES: 6
 NAME: Toohey Kimberlin M
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02481.1453-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 1576
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 MOLECULE TYPE:
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS
 1505
 541
 499
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 I Street, N.W., Suite 700 CITY: Washington STATE: D.C. COUNTRY: USA
 FILING DATE:
 APPLICATION NUMBER:
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 INFORMATION:
 20005-3315
 Application
 8.2%;
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Conservative
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 US/08501572
 US/08/501,572
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 Score 150.4; DB 3; Pred. No. 5.3e-28; 0; Mismatches 641;
 Version
 DB 3;
 #1.30
 And Their Use.
 Length
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; TOPOLOGY: Linear
; MOLECULE TYPE: DNA (gen
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 Query Match
Best Local Similarity
Matches 577; Conserv
 Sequence 6, Application Patent No. 6063766
 TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 GENERAL INFORMATION:
 APPLICANT:
APPLICANT:
 REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: March 18,
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
 APPLICANT: Grundeman, Dirk
APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport protein Which Effects The
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and\or Pharmaceuticals,
TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
NUMBER OF SEQUENCES: 6
 ATTORNEY/AGENT INFORMATION:
NAME: O'CONNOT, Steven P
REGISTRATION NUMBER: 41,
 CORRESPONDENCE ADDRESS:
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 STATE: D.C.
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ZIP: 20005-33
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
 STREET: 1300 I S CITY: Washington
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 LENGTH:
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 ADDRESSEE:
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 E: Finnegan, Henderson, Farabow, Garrett & Dunner, 1300 I Street, N.W., Suite 700
 8.2%;
ilarity 46.9%;
Conservative
 Koepsell,
 PatentIn Release #1.0,
 (202)408-4000
 DNA (genomic)
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 US/09/040,444
|8, 1998
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GENERAL INFORMATION:

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US-08-647-397-1
 Query Match
Best Local
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 TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2102 base pairs
 FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B080
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield
 FRAGMENT TYPE:
ORIGINAL SOURCE:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 APPLICANT: Beier, David R. APPLICANT: Brady, Kevin P. TITLE OF INVENTION: OSTEOC
 FEATURE
 ANTI-SENSE:
 HYPOTHETICAL:
 TOPOLOGY: li
 TELEPHONE: 617-720-3500
 CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES:
 CITY: Boston
STATE: MA
COUNTRY: USA
 677
 189
 621
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 ADDRESSEE: WOLL, GALLER STREET: 600 Atlantic Avenue
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 NAME/KEY:
 ORGANISM:
 STRANDEDNESS:
 APPLICATION NUMBER:
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 nucleic acid
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 Score 124.8; DB 2;
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

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Sequence 14, Application US/08232463
Patent No. 5670367
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Foley & Lardner 00 Diagonal Road, Suite 500

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 US-08-232-463-14
 Query Match 2.9%; Score 53; DB 1; Best Local Similarity 6.2%; Pred. No. 0.0012; Matches 26; Conservative 218; Mismatches 1
 INFORMATION FOR SEQ ID NO: 14:
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 REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
1416 YYYYYYYYYYYYYYYYYYGTACCAAATTCTTCTATCTCTTTAACTACTTGCATAGA 1472
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 IMMEDIATE SOURCE:
 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 STRANDEDNESS: Sin
 LENGTH: 7210 LLENGTH: 7210 LLE
 TELEFAX: (703 TELEX: 899149
 COMPUTER: IBM PC
OPERATING SYSTEM:
 ADDRESSEE: Foley
STREET: 1800 Dia
CITY: Alexandria
 CLONE:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION: 435
 FILING DATE:
 APPLICATION NUMBER:
 COUNTRY: USA
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 (703)683-4109
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SYSTEM: PC-DOS/MS-DOS
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 EP 91 114 300.6
 US/07/935,313
 US/08/232,463
 30472/114 IMMU
 DB 1; Length 7218;
 173; Indels
 0;
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 PCT-US95-14418-3
 PCT-US95-14418-3
 Query Match
Best Local Similarity
Matches 205; Conserv
 Sequence 3, Application GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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 SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
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 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TELEFAX: 25-3856
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 TOPOLOGY:
 STRANDEDNESS: single
 REFERENCE/DOCKET NUMBER:
 REGISTRATION NUMBER:
 CLASSIFICATION:
 FILING DATE:
 APPLICATION NUMBER:
 COUNTRY:
 CITY: Chicago
 STREET:
 NAME: Gass,
 LENGTH:
 ADDRESSEE:
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 6300 Sears Tower,
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 CDS
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 Marshall,
 David A.
 DNA (genomic)
 2.9%;
 DNA
51
 PC/TUS9514418
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Tower, 233
 PCT/US95/14418
 38,153
 Encoding a Thermostable DNA Polymerase Enzyme
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 0; Mismatches 233;
 Score 52.2; DB 5
Pred. No. 0.0011;
 28003/32330
 Gerstein, Murray &
South Wacker Drive
 DB 5;
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PCT-US95-15327-3
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; GENERAL INFORMATION:
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 CT-US95-15327-3
 Matches
 Query Match
Best Local Similarity
 TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 2800
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 NUMBER OF SEQUENCES: 5
 ATTORNEY/AGENT INFORMATION:
 TITLE OF INVENTION:
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 APPLICANT:
 MOLECULE TYPE:
 334
 454
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 TOPOLOGY: lin
 94
 CLASSIFICATION:
 CITY: Chicago
 APPLICATION NUMBER:
 COUNTRY:
 NAME/KEY:
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 ADDRESSEE:
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 Application PC/TUS9515327
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 6300 Sears Tower,
 United States of America
 Conservative
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 Marshall, O'Toole,
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Thermus Flavus DNA Polymerase
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 2.9%;
 PCT/US95/15327
 0
 28003/31716
 Score 52.2; DB 5; Pred. No. 0.0011;
 Mismatches
 Gerstein, Murray & South Wacker Drive
 Version
 233;
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 Length 1794;
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 RESULT 13
PCT-US95-14418-1
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 PCT-US95-14418-1
 Sequence 1, Application PC/TUS9514418 GENERAL INFORMATION:
 Best Local Similarity Matches 205; Conserv
 Query Match
 INFORMATION FOR SEQ ID NO:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'To
STREET: 6300 Sears Tower,
 1348
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
 FEATURE:
 TOPOLOGY: 1: MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION: NAME: Gass, David A.
 COMPUTER READABLE FORM:
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 COUNTRY:
 CITY: Chicago
 REFERENCE/DOCKET NUMBER:
 APPLICATION NUMBER:
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 United States
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 DNA (genomic)
 single
 2.9%;
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51
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 38,153
 PCT/US95/14418
 Encoding a Thermostable DNA
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 534
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South Wacker Drive
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 Sequence 1, Applicati GENERAL INFORMATION: APPLICANT:
 Query Match 2.9%;
Best Local Similarity 46.5%;
Matches 205; Conservative
 TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
 NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
 1705
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 1585
 1525
 1465
 FEATURE:
 MOLECULE TYPE:
 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION:
 1765 CGGGACCAGCTGGAAAGGGTG 1785
 454
 394
 334
 274
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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 TOPOLOGY:
 STRANDEDNESS:
 CLASSIFICATION:
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 APPLICATION NUMBER: PCT/US95/15327
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 Chicago
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 Illinois
 Application PC/TUS9515327
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 linear
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 DNA (genomic)
 single
 Biologically Active Fragments
Thermus Flavus DNA Polymerase
51
 534
 Score 52.2; DB 5;
Pred. No. 0.0013;
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 Gerstein, Murray &
South Wacker Drive
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 US-09-103-840A-2
 APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR THE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
 CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
 Query Match
Best Local (
 GENERAL INFORMATION:
 Sequence 2, Application US/09103840A Patent No. 6294328
 Best Local Similarity 48.4 Matches 137; Conservative
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 1860445 ttcggcggcaacccggtctgcgccgcggcgcgctggcggtgctacgggtgctggcgagc 1860504
 FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
 LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
 1465
 1765 CGGGACCAGCTGGAAAGGGTG 1785
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## ALIGNMENTS

REFERENCE AUTHORS SOURCE ORGANISM RESULT BG332869 LOCUS COMMENT FEATURES DEFINITION KEYWORDS ACCESSION ERSION TITLE JOURNAL source Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 754)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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 Email: cgapbs r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D.,
cDNA Library Preparation: Michael J. Brown
Toshiyuki and Piero Carninci (RIKEN)
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M.D., Ph.D. Brownstein (NHGRI), Shiraki

Consortium (LLNL)

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 (gtcgag
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 Вb
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 COMMENT
 SOURCE
 Q
 δÃ
 밁
 В
 KEYWORDS
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 Query Match
Best Local S
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 ORGANISM
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Clone distribution: MGC clone distribution information can
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http://image.llnl.gov
Plate: LLAM11663 row: p column: 10
 Email: cgapbs-r@mail.nih.gov
Tissue procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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 Similarity
 quality sequence stop:
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 1;
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420

360

480

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 Вb
 BASE COUNT
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 В
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 Вþ
 δÕ
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 FEATURES
 COMMENT
 ACCESSION
 DEFINITION
 Query Match
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National Institutes of Health, N
Unpublished (1999)
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 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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 mRNA sequence.
BE546219
 Contact: Robert
 Eukaryota;
 Homo sapiens
 BE546219.1 GI:9774864
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information

Clone distribution: MGC clone distribution information
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 cDNA Library Preparation: Life Technologies, I con Library Arrayed by: Incyte Genomics, Inc.
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 Strausberg, Ph.D.
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 Score 573.4; 1
Pred. No. 6.9e
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 Homo
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JOURNAL
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BI647860
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 COMMENT
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Den
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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National Institutes of Health, |
Unpublished (1999)
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BI647860
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 BI647860.1
 Contact: Robert Strausberg, Ph.D.
 Eukaryota; Metazoa;
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Mus musculus cDNA clone
 Mammalian
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NotI;

Gene

Collection (MGC)

Deng

Ph.D.

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Murinae; Mus

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밁

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SOURCE
ORGANISM
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 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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http://image.llnl.gov
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 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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1 (bases 1 to 806)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Primer:

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Mammalia; Eutheria; R
1 (bases 1 to 800)
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
 mRNA sequence.
BI683731
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603306292F1 NCI_CGAP_Mam6
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
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National Institutes of Health, Mammalian
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 CDNA
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BF783848
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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 BASE COUNT
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 Email: capabs-r@mail.nih.gov
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National Institutes of Health, Mammalian Gene
Unpublished (1999)
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 Unpublished (2000)
Contact: Smith TPL
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 USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366 Fax: 402 762 4390
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 Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community.
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
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 BG087364
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EST.
 Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
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 Mus musculus
 National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820,
 Laboratory of Genetics
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1 NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green,
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 Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complant and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Technologies. Note: this is a NCI_CGAP Library. |"
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